Perfect score:

Sequence:

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Scoring table:

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paragporal crystal protein cry4Aal - Bacillus thuringiensis subsp. israelensis

N;Alternate names: paragporal crystal protein cryIVA

N;Alternate names: paragporal crystal protein cryIVA

C;Species Bacillus thuringiensis subsp. israelensis

C;Accession: A56858; S48691

R;Ward, B.S.; Bllar, D.J.

Nucleic Acids Res. 15, 7195,

A;Title: Nucleotide sequence of a Bacillus thuringiensis var. israelensis gene encoding

A;Reference number: A26858; MUID:88015571; PMID:2821500

A;Reference contact and a sequence of a Bacillus thuringiensis var. israelensis gene encoding

A;Reference number: A26858

A;Molecule type: DNA

A;Residues: 1-1180 cMARA

A;Coss.references: UNIPROT:P16480; UNIPRAC:UPI000016EA42; GB:Y00423; NID:940351; PIDN::

A;Note: the authors translated the codon GCA for residue 308 as Thr

R;Nishimcto, T.; Yoshisue, H.; Ihara, K.; Sakai, H.; Komano, T.

R;Nishimctional analysis of block 5, one of the highly conserved amino acid sequence on number: 848691; MUID:94307434; PMID:7913448
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A;Molecule type: DNA
A;Residues: 667-676 <NIS>
A;Cross-references: UNIPARC:UP1000017819A
C;Superfamily: Parasporal crystal protein
C;Keywords: delta-endotoxin
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Result Š

Page 2

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1414 ------AGTAATAAATTAACATATTCAGCTGGGGAATTTATCTAATGATAAAAA 1464
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ValThrThrTyrLysLysGlyLeuAsnLeuIleLysThrThrProAspSerAsnLeuAsp
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375 ThrProAsnAsnPhePhe---ThrSerHisTyrAsnMetPheHisTyrThrLeuAspAsn
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IlsesrGlnLysSerSerValPheGlyAsnHisAsnValThrAspLysLeuLysSerLeu
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LysPheGluAlaTyrLeuLysAsnArgGlnPheAspTyrLeuGluPro---LeuPro
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                                                         TTACTACCTATTTATGCGCAAGCTGCTAATTTTCATTTAAATTTTACAACAAGGTGCT
                                                                                                                                                                       ACATCAGATGACTATTATAAACTTTTAAAAGAAAATATACCTAAATATAGTAACTATTGT
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AATGATTTTATTCGAGAAATACCT-
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c;Species Bacillus thuringiensis
c;Species Bacillus thuringiensis
c;Species Bacillus thuringiensis
c;Date: 19-Ual-1996 #sequence_revision 19-Jul-1996 #text_change 05-Oct-2004
c;Accession: I39870
Agric. Biol. Chem. 52, 873-878, 1988
A;Title: Cloning and nucleotide sequences of the two 130 kDa insecticidal protein genes
A;Reference number: I39869
A;Accession: I39870
A;Accession: I39870
A;Residus: preliminary; translated from GB/EWBL/DDBJ
A;Molecule type: DNA
A;Residus: 1-1180 <RES>
A;Residus: 1-1180 <RES>
A;Cross-references: UNIPROT:P16480; UNIPARC:UP1000001B1F; GB:D00248; NID:g216289; PIDN:C;Superfamily: Parasporal crystal protein
C;Keywords: delta-endotoxin
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AsnLysAsnGluTyrGluThrLeuAsnAlaSerGlnLysLysLeuAsnIleSerAsnAsn 25
                              -------TyrThrArgTyrProlleGluAsnSerProLysGlnLeuLeuGlnSer
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ThrValLeuThrGlyPheGlyPheThrThr------ProLeuGlyLeu-----
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gg	360 AspProTyrAspIlePheSerPheThrGlyAsnGlnMetAla373	į
ò	1219 AGATCTACTTATGCTACGACAGGAACTGAAATTATATGAGAAAGAA	<u> </u>
qq	SlyAlaValHisGlyAsnIle 392	}
È	1273CCACCCACACAAAACTTTAATACCATTTGAATCCTATAAAGTT 1317	3 8
QQ Q	393 IleSerGlnAspThrSerLysValPheProPheTyrArgAsnLysProlleAspLysVal 412	RESUI
È	TCAATTGTAACTGATAGACAAGTAACTCCTACTTCCCTAACATATACTTTACA 1377	USBS
ብ	GluileValArgHisArgGluGluileValArgHisArgGluTyrSerAsp 422	N,Al C,Spe
È	ATTAATCAAATTGAACTTTATTTAAATAATTCACCTAGTAATAAATTAACATATTCAGCT 1437	C;Da
셤	423 ilelleTyrGluMetilePhePheSerAsnSerSerGluValPheArgTyrSerSer 441	R,Chi Bur.
È	GGGGGGAATTTATCTAATGATAAAAAACAACTGATTTTCAATTTCCTGTAAAAAAAGAC 1497	A;Ti
qq	442 AsnSerThrIleGluAsnAsnTyrLysArgThrAspSerTyrMetIleProLysGlnThr 461	A; AC
ò 1	TGTAAACCAATTATTAATCCAAATTGTTTACCAAGCTATAATAGTTATAGTCATATTTA 1557	A;Rei
a ,	1rpLy8	Gene
हे ह	TCCCAGTITICITIAITITAATIAITICCTATAAAATINGGATIAGGCGCTAAATATATATAT 1617	A;T1
G	222	A; Mo
È	1677	A; Re
qq	508	A; Cr
ò	1678 ATAATTACAATGATCCCAGCAATCAAAGGTAACAGTCTTGATACAAACTCTAAGGTAATT 1737	A MO
QQ	528	A;Cr
È	1738 GAAGGACCTGGTCATACAGGAGGAACTTGGTTTATTTACAAAGTCAAGGGCGTTTAGAG 1797	, X
qq	546	A;Ti
È	T 1854	A; Ac
dg G	547 PheArgValArgPheLeuLysAsnValSerArgGlnTyrGlnValArgIleArgTyrAla 566	A ; Re
È	1914	R; Ser
qq	567 Thrashala	A; Ti
È	1915 ATACCACCICAACGACTCAACAACTTTTTTGGTACAAATTATAATAATTTA 1968	A; Ac
đ	LeuproserthrThrSerArgGlnAsnProAsnAlaThrAspLeu 600	A; Wo
È	CAATACGGGGATTTTGGGGTATTTCCAATTTCCAAGTACAGTA	A; Cr
අු	601 ThrTyrAlaAspPheGlyTyrValThrPheProArgThrValProAsnLysThrPheGlu 620	Mol. A;Ti
È	GAAACATACCATTTATATTTAATCGTGCAGATGTA 2061	A;Re
qq	GlyThrProAsnHis 635	A; St
È	2121	A;Re
q	654	C;Co
È	2157	C; Ke
g	655 AspTyrThrdluLysdlnAsnIledluLysThrdlnLysIleValAsnAspLeuPheVal 674	Alig
ò	2166	Scor
qq	 easpSerMetalaValLysLysAlaArgLysValVal 694	Best

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"asporal crystal protein cry4Bal [validated] - Bacillus thuringiensis subsp. israelens liternate names: delta-endotoxin Bt8; insecticidal protein ISRH3; mosquitocidal 130K ppecies: Bacillus thuringiensis subsp. israelensis sactorial and subsp. israelensis nastupornchai, W.; Hoefte, H.; Surinck, J.; Angsuthanasombat, C.; Vaeck, M. J. Blochem. 173, 9-16, 1988 curinck, J.; Angsuthanasombat, C.; Vaeck, M. itle: Common features of Bacillus thuringiensis toxins specific for Diptera and Lepid eference number: 800398; WUID:8818534; PMID:2833395 coession: 800398
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ross-references: UNIPROT:P05519; UNIPRARC:UP10000001B1D; EWBL:X07423; NID:g40353; PIDN
ross-references: UNIPROT:P05519; UNIPARC:UP10000001B1D; EWBL:X07423; NID:g40353; PIDN
amamacot. T.; Watkinson, I.A.; Kim, L.; Sage, M.V.; Stratton, R.; Akande, N.; Li, Y.;
e 66, 107-120, 1988
itle: Nucleotide sequence of the gene coding for a 130-kDa mosquitocidal protein of B
eference number: JT0315; MUID:88329719; PMID:2901387
ccession: A37587
esidues: 1-50, DV, 52-64, S', 66-192, PHKCTRANYY, 202-204, C', 207-363, IVVQIXLIKEN', 374,
residues: 1-50, DV, 53-64, S', 66-192, PHKCTRANYY, 202-204, C', 207-363, IVVQIXLIKEN', 374,
residues: 1-50, DV, 53-64, S', 66-192, PHKCTRANYY, 202-204, C', 207-363, IVVQIXLIKEN', 374,
residues: 1-50, DV, 53-64, S', 66-192, PHKCTRANYY, 202-204, C', 207-363, IVVQIXLIKEN', 33-43,
reserve references: UNIPARC:UP1000016EA34; GB:M20242; NID:g142737; PIDN:AAA22337.1; PID:
ccession: JT0315
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lote: the majority of sequence differences are consistent with frameshift errors
ungpradubkul, S.; Settasatien, C.; Panyim, S.
leic Acids Res. 16, 1637-1638, 1988
litle: The complete nucleotide sequence of a 130 kDa mosquito-larvicidal delta-endotox
leference number: A28541; MUID:88157738; PMID:2831510
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Iolecule 1-204, "R', 206-1136 <TUN
Iolecule 1-204, "R', 1988
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2167 AATACATTTTTCACAAATCATACAAAAATACTTTAAATATAGAAGCCACAAACTATGAT 2226
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1087 CCCAATCTCGCTATAATGGAATATAATTAACACGTTCAGGGCTTAGATTATTTTCATTT 1146		1249 ATTATATATGAGAAAGAACAGGTCCACACAACAAAAACTTTAATACCATTTGAATCC 1308	377 AGNValTyrLyGThrSerIle	TTAACATATTCAGCTGGGGGAATTTATCTAA -::	1456GATAAAAAACAACTGATTTTCAATTTCCTGTAAAAAAGACTGT 1500 :::	AAACCAATTATTAATCCAAATTGTTTACCAAGCTATAATAGTTATAGTCATATTTTATCC	CAGTITICITIATITAATIATICCIAIAAAATIGGATIAGGGCIAAATATA :::::::::::::::::::::::::::::::		GATAAAATAATTACAATGATCCCAGGAATCAAAGGTAACAGTCTTGATACAAACTCTAAG	GTAATTGAAGACCTGGTCATACAGAGGAACTTGGTTTATTTA	CAAGGGGGTTTAGAGATTACATGTAGAACTCCTAATTCTACACAATCT :: LeuSerGlyArgMetGlulleGlnCysLysThrSex1lePheAsnAspFroThrArgSer	1831 TATTACATTAGACTTCGATACGCTACAATGGTGCAGAATACTCTTCCTAATATATCT 1890 ::: ::	1891 CTTACAATACCAGGAGTAATAGGAATACCACCTCAACGACTCAACAACACTTTTTCTGGT 1950	1951 ACAAATTATAATAATTTACAATACGGAGATTTTGGGTATTTCCAATTT 1998	1999 CCAAGTACGTAACGTTAACTTTAAATCGAAACATACCATTTATATTTAATCGT 2052 ::: :: :::	
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Query Match: 20.79% Indels: 130 DB: 33 US-10-782-570-1 (1-2235) × USBSB1 (1-1136) Qy 79 CATTCTAGATACCTTACACAAATAATCCAAATCAACCATTACAAAACACAAATTACAAA 138	Db 2 AsnSerGlyTyTriPlinglandsDeuGlnGlySerMetLysAsnThINININININININININININININININININININ	199 AGTGCTGATACAATTGCTGCAGTTAGTGCAGGTACTATTGTATCCGGTACTCTGTTAGCC ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: :::	OY 259 GGTATAGGTGGGCTCACTTCTATATCGGACCATAGGATATAGGTGCTATAATAATA 318	71SerAlaValLeuProlleLeuTrpProThrAsnThrProThrProGluArgVal 376 TGGACACAATTTATTAAAATGCGAGAAATTTTTTGTTGATACACCGTTAACAGAAAGCATA	UD 89 TrpabnasprhemecintabnintGiyasnLeulleaspGinintValintAlalyrVal 108 Qy 436 AAACAGCTAAAGTTACAAACTTTAGAAGGATTTAGAAATATTACAAAAGCTATAATA 495 Db 109 ArcThraspAlaAsnAlaLvaMetThrValValLvalAsnGintVarhyrThr 128	496 GCATTAGATTAGAAATTAAAAAGACTACAAGCTCCTGGATTACCACCATCATCA 129 LygPheAsnThrTrpLysArgGluProAsnAsnGln	Qy 556 GCATTACAACAAGCTGCCTTGACTCTTAAAATACGATTTGAGAATGTTCACAATGATTTT 615 11 :: ::	Qy 616 ATTCGAGAAATACCTGGTTTCCAACTTGAAACGCTATTACTACCT 669 15:		Oy 730 GATGAATGCAGATATACATCCTTCACAAATTGAACCTAATGCTGGAACATCAGAT 789	Oy 790 GACTATTATAAACTATATACCTAAATATACTAAATATAGTAACTATTGTGCAAATACC 849	Qy 850 TATAGAGAAGGACTAAATAAACTTCGAAACGAACCTAATATGAGATGGAGTATATTTAAT 909 L	910 GATTATCGAAGATATAGACTATTACTGTATTAGATACTATCGCTCAATTTTCTTTTAT	Oy 970 GATATAAAGAGATACAAAGATTCAATAGGAAGAATAGGGGGTTAAAACTGAACTT 1026	1027 ACAAGAAATTTATACAACTGAAATAAATTTTGACCGTCTTACTTA	Db 288 ThrArgGluileTyrThrAlaLeuValGluSerProSerSer 301

i 418 CCGTTAACAGAAAGCATAAAACAGCTAAAGTTACAAACTTTAGAAGATTTAGACAAATA 4 ::: ::: :::	The control of the co		598 AATGTTCACAATGATTTTATTCGAGAAATACCTGGTTTCCAACTTGAAACTTATAAAACG 6 1::	658 CTATTACTACCTATTTATGCGCAAGCTGCTAATTTTCATTTAAAATTTACAACAAGGT 7		221 GlnValPheGlyGluĠluTrpGlyTyr221 GlnValPheGlyGluĠluTrpGlyTyr 2 778 GGAACATCAGATGACTATTATAAACTTTTAAAAGAAATATACCTAAATAT 8	::: ::: ::: ::: ::: 230SerSerGluAspIleAlaGluPheTyrGlnArgGlnLeuLysLeuThrGlnGlnTyr 2	829 AGTAACTATTGTGCAAATACCTATAGAGAGGACTAAATAAA	889 ATGAGATGGAGTATATTAATGATTATCGAAGATATATGACTATTACTGTATTAGATACT 9 269 AGRADATATTAGATAATGATTAATGATACT 9 269 AGRADATAGATAGATAGATAGATAGATAGATAGATAGATAGAT	ATCGCTCAATTTTCTTTTTATGATATAAAGAGATACAAGATTCAATAGGAATAGGT		1009 GGCATTAAAACTGAACTTACAAAAATTTATACAACTGAAATAAAT	1069 ACTTACCTTGAAATTCAACCCAATCTCGCTATAAATGAATATAATTTAACACGTTCAGGG 1	CTTAGATTATTTTTAGATGAACTTATATTTTATACAAAA	341HibleukheabpTyrbeuargGilyileGiukheHibinkargLeuargkroGilyiyr 3 1174AATGAAACGTACGGGAATCGTTTAGTTGGTATTGCGAATCGT 1	SerGlyLysAspS	1216 AATAGATCTACTTATGCTACGAACTGAAATTATATATATA	1276 CCCACAACAAAAACTTTAATACCATTTGAATCCTATAAAGTTTCAATTGTAACTGATAGA 1 	1336 CAAGTAACTCCTACTTCCCCTTTTCCTAACATATACTTTACAATTAAT 1 :: ::	1384 CARATTGRACTTTATTRAATAATTCACCTAGTAATTAATTAACATATTCA 1
8 8 8	6 8 8	-	& 8	& A	<i>ò</i>	6 B	ପ୍ର	PIDN OY	8 6	à	QQ (충 옵	8 8	& f	8 ò	: 名	8	& 8 8	<i>></i> 옵	% a
Db 615 LeuasnMetThrSerAsnAsnGlnValileIleasparglieGluIleIleProlleThr 634 Qy 2110 TCCTCTGTACGCCAAAATAGAGAAAAATTAGAAACTATCCAAACAAA	2170 ACATTTTCACAAATCATACAAAAAATACTTTAAATATAGAAGCCACAAACTATGATATTTTCACAAATCATACAAAAAAAA	2230 GMT 2232	Db 675 Agp 675 RESULT 5	S10228 parasporal crystal protein cry3Bal - Bacillus thuringiensis (fragment) N;Alternate names: coleopteran-active parasporal crystal protein; delta-endotoxin C;Species: Bacillus thuringiensis	<pre>C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 05-Oct-2004 C;Accession: S10228 R;Sick, A.; Gaertner, F.; Wonq, A.</pre>	Nucleic Acids Res. 18, 1305, 1990 A;Title: Nucleotide sequence of a coleopteran-active toxin gene from a new isolate of A;Reference number: S10228; MUID:90206811; PMID:2320431	A.Accession: S10228 A.FStetus: translation not shown A.Molecule trae: DNA	RC:UPI0000126C13; EMBL:X17123; NID:g40258;	A;Gene: cryIIIB : C;Superfamily: Parasporal crystal protein C;Keywords: delta-endotoxin; toxin	Alignment Scores: Pred. No.: 1.73e-38 Length: 659 Score: 706 00 Matches: 216	larity: 44.27% imilarity: 28.80%	17.92* Indels: 2 Gaps:	US-10-782-570-1 (1-2235) x S10228 (1-659) Qy	ProAsnAsnArgs		Qy 118 TTACAAAACACAAATTACAAAGAGTGGCTCAATATGTGTGTCAAGGGAATACACAATATGGT 177	GATAATTTCGAGACATTTGCTAGTGCTGATACAATTGCTGCAGTTAGTGCAGGTACTATT	238 GTATCCGGTACTCTGTTAGCCGGTATAGGTGGGCTCACTTCTATATCCGGACCGATAGGA	Db 80 ValValdlyGlnIleLeuGlyValValdlyValPro 91 Qy 298 ATAATAGGGGTATAATAATATTTTTGGACCGGGGGA 357	Db 92 PheAladiyAiaLeuThrSerPheTyrGlnSerPheLeuAsnAlaIleTrpPrOSer 110 Qy 358 GAACAAGACAAAACAGTATGGACACAATTTATAAAATGGGAGAAATTTTGTTGATACA 417 Qy

1.64e-37 691.00 691.00 81milarity: 28.26* h: 17.54*	US-10-782-570-1 (1-2235) x 139811 (1-652) QY	CACAAATAA :::	121 CAAAACACAAATTACAAAGAGTGGCTCAATATGTGTCAAGGGAATACACAATATGGT :::	38 GluGluLeuAsnTyrLysGluPheLeuArgMetThrGluAspSerSerThrGluValLeu 178 GATAATTTCGAGACATTTGCTAGTGCTGATACAATTGCTGCAGTTAGTGCAGGTACT	58 ABPABNSEFINIYALLYBABPALAVALGIYINKGIYLLE 235 ATTGTATCCGGTACTCTGTTAGCCGGTATAGGTGGCCTCACTTCTATATCCGGACCGATA	Db 71 SerValValGlyGlnIleLeuGlyValValGly	Db 83 ProPheAlaGlyAlaLeuThrSerPheTyrGlnSerPheLeuAsnThrIleTrProSer 102 Qy 355 GGAGAACAAGACAAAACAGTATGGACACAATTTATTAAAATGGGAGAAATTTTTGTTGAT 414		120 LystyslleGluGluTyralaLysSerLysAlaLeuAlaGluLeuGlnGlyLeuGlnAsn	CY 475 ATATTACAAAGCTATAATACAGCATTAGATGAGAAAAATTAAAAAGACTACAAGCT 534 ::: ::: Db 140 AanPheGjuaanTvvValAanalaLenAanSerTrolveLva153	535 CCTGGATTACCACCATCATCAGCATTACAACAAGCTGCCTTGACTCTTAAAATACGATTT	Db 154ThrProLeuSerLeuArgSerLysArgSerGlnAspArgIleArgGluLeuPhe 171 Qy 595 GAGAATGTTCACAATTATTCGAGAAATACCTGGTTTCCAACTTGAAACTTATAAA 654	655 ACGCTATTACTACCTATTTATGCGCAAGCTGCTAATTTTCATTTAAATTTATTACAAAA	Db 192 ValieuPheieuProThrTyrAlaGlnAlaAlaAsnThrHisieuLeuLeuLeuLveABP 211 Oy 715 GGTGCTGAATTGGCTGAATGGAATGGAATACATACATCCTTCACAAATTGAACCTAAT 774	212	Qy 775 GCTGGAACATGAGATGACTATTATAAAGAAAAGAAAATATACCTAAATATAGTAAC 834	Oy 835 TATTGTGCAAATACCTATAGAAAGGACTAAATAAACTTCGAAACGAACCTAATATGAGA 894 1::	895 TGGAGTATATTJAATGATTATCGAAGATATATAGTGATTACTGTATTAGATACTATCGCT	DD 263 TrpValLy8PheAsnArgPheArgArgGluMetThrLeuThrValLeuAspLeulleVal 282
Qy 1435 GCTAAA 1464 ::	1525 TTACCAAGCTATAATAGTCATATTTTATCCCAGTTTTCTTTATTTA	Oy 1585 TATAAAATTGGATTAGGGCTAAATATATATACAGGTGCATTAGGATGGACACAGT 1644 	Qy 1645 AGTGTTAATAGAAATAGCAATACCAGAATAAATAATTACAATGAATCAAA 1704 :::	Qy 1705 GGTAACAGTCTTGATACAACTCTAAGGTAATTGAAGGACCTGGTCATACAGGAGGAAAC 1764	Qy 1765 TIGGTTTATACAAAGTCAAGGCGTTTAGAGATTACATGTAGAACT 1812 ::::: ::: :::	Oy 1813 CCTAATTCTACACAATCTTATTACATTAGACTTTCGATACGTACAAATGGTGCTGGAAAT 1872	1873 ACTCTTCCTAATATATCTCTTACAATACCAGGAGTAATAGGAATACCACCTCAACGACTC	Qy 1933 AACAACATTTTCTGGTACAATTATAATAATTTACAATACGGAGATTTTGGG 1986	Db 594 Agnin 1987	614 TyrdlnThrPheAbpPheAlaThrSerAsnSerAsnMetGlyPhe 628	Qy 2041 ATATTAATCGTGCGAGAT	Qy 2077 ATCATTGATAATTGATTTATACCAATT 2106 	RESULT 6 139811 parasporal crystal protein cry3Bbl - Bacillus thuringiensis	NyAlternate names: parasporal crystal protein cryl11B2 C;Species: Bacillus thuringiensis C;Date: 19-Jul-1996 #sequence revision 19-Jul-1996 #text change 05-Oct-2004	C;Accession: 139811 R;Donovan, W.P.; Rupar, M.J.; Slaney, A.C.; Malvar, T.; Gawron-Burks, M.C.; Johnson, T.E Annl Environ Mirrohiol 68 1921-1927 1982	A. Title: Characterization of two genes encoding Bacillus thuringiensis insecticidal crys A; Reference number: 139811; MUID: 93119147; PMID: 1476436 A; Accession: 139811	A;Stetus: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Mesidues: 1-652 <res> A;Cross-references: UNIPROT:Q06117; UNIPARC:UPI0000126C14; GB:M89794; NID:g142729; PIDN:</res>	C;Genetics: A;Gene: cryIIIB2 C;Superfamily: Parasporal crystal protein	Alignment Scores:

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955 CAAITITICTITITAAAGAGATACAAAGATTCAATAGGAAGAATAGGGATT 1014 283 Leupheprophetytaspill	AAAACTGAACTTACAAGAAATTTATACAACTGAAATAAAT	LysThrGluLeuThrArgAspllePheThrAspProllePheSerLeuAsnThrLeu	1075 CTTGAAATTCAACCCAATCTCGCTATAATGGAATATAATTAACACGTTCAGGGCTTAGA 1133 	TTATTTTCATTTTTAGATGAACTTATATTTTATACAAAA	::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::::	AATGAAACGTACGGAAATCGTTTAGTTGGTATTGCGAATCGTAATAGA	354 LybabgberPheAbnlyrIrpSerGlyAbnlyrValGluIhrargFroser 370 1222 TCTACTTANGCTACGACAGGAACTGAAATTATATATATGGAGAAAGAACAGGTCCACCCAC		CCATTTGAATCCTATAAAGTTTCAATTGTAACTGATAGACAA	391 GlnLysArgThrile 404	ACTCCTACTTCCCTAACATATACTTTACAATTAATCAAATT	AlaAsnThrAspValAlaAlaTrpProAsnGlyLysValTyrLeuGlyValThrLysVal	1390 GAACTTTATTTAAATAATTCACCTAGTAATTAATTAACATATTCACTT 143 425 AspheSerGlnTvrAspAspGlnLvaA ::: 425 AspheSerGlnTvrAspAspGlnLvaAnJuThrSerThrGlnThrTvrAspSerLva 444	GGGGGGAATTTATCTAATGATAAAAAACAACTGATTTTCAATTTCCTGTAAAA		1492 AAAGACTGTAAACCAATTATTAATCCAAATTGTTTACCAAGCTATAATAGTTATAGTCAT 1551	463 ThrThrAspGluProLeuGluLysAlaTyrSerHis 474	1552 AITTTATCCCAGITTTCTTTATTATTATTCCTATAAAATTGGATTAGCGCTAAATATA 1611	TyrAlaGluCysPheLeuMetGlnAsp	1612 TTATATACAGTGCATTAGGATGGACACAGAGTGTTAATAGAAATAATGCATATCA 1671	493 PhePheThrTrpThrHisArgSerValAspPhePheAshThrIleAsp 508	1672 GATAAAATTACAATGATCCCGGCAATCAAGGTAACAGTCTTGATACAAACTCTAAG 1731	509 AlaGluLysileThrGlnLeuProValValLysAlaTyrAlaLeuSerSerGlyAlaSer 528	1732 GTAATTGAAGGACCTGGTCATACAGGAGGAACTTGGTTTATTTA	529 IleIleGluGlyProGlyPheThrGlyGlyAsnLeubheLeuLysGluSerSerAsn 548	1780 AGICAAGGGGTITIAGAGATTACATGTAGAACTCCTAATTCTACACAATCTTATTACATT 1839	PheLysValThrLeuAsnSerAlaAlaLeuLeuGlnArgTyrArg	1840 AGACTTCGATACGCTACAAATGGTGCTGGAAATACTCTTCCTAATATATCTCTTACAATA 1899	569 ArgileArgTyrAlaSerThrThrAsnLeuArgLeuPheVal 582	1900 CCAGGAGTAATAGGAATACCACCTCAACGACTCAACAACTTTTTCTGGTACAAATTAT 1959	583	1960 AATAATTTACAATACGGAGATTTTGGGTATTTCCAATTT 1998
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rasporal crystal protein cry7Aal - Bacillus thuringiensis
Alternate names: parasporal crystal protein cryIIC
Species: Bacillus thuringiensis
Accession: A48944
Accession: A48944
Lambert, B.; Hofte, H.; Annys, K.; Jansens, S.; Soetaert, P.; Peferoen, M.
Ph. Environ. Microbiol. 58, 2536-2542, 1992
Title: Novel Bacillus thuringiensis insecticidal crystal protein with a silent activit
Reference number: A48944; MUID:92384571; PMID:1514800
Contents: B75137
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                                                                                                                                      1999 CCAAGTACAGTAACATTACCTTTAAATCGAAACATAACCATTTATATTTAATCGTGCAGAT 2058
TCTAACAGAAATATTGATCATTCT---AGATACCCTTACACAAATAATCCAAATCAACCA 117
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|112 AspGlnLysIleGluGluTyrValArgAsnLysAlaIleAlaGluLeuAspGlyLeuGly 131
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|SerAsnArgThrLeuAsnAsnSerLeuAsnTyrProThrGlnLysAlaLeuSerProSer 31
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ò	2227	ATTGAT 2232	
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RESULT 8			

8 6 6 6

8686

RESULT 8
140589
parasporal crystal protein cry8Cal - Bacillus thuringiensis
N;Alternate names: parasporal crystal protein cry1II
C;Species: Bacillus thuringiensis
C;Species: Bacillus thuringiensis
C;Species: Bacillus thuringiensis
C;Species: Bacillus thuringiensis
C;Sacession: 140589
R;Sato, R.; Takeuchi, K.; Ogiwara, K.; Minami, M.; Kaji, Y.; Suzuki, N.; Hori, H.; Asano
Curr. Microbiol. 28, 15-19, 1594
A;Title: Cloning, heterologous expression, and localization of a novel crystal protein g
A;Title: Cloning, heterologous expression, and localization of a novel crystal protein g
A;Accession: 140589
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1160 eRESA;Cross-references: UNIPROT:Q45706; UNIPARC:UPI0000126CFE; EMBL:U04366; NID:g532523; PID:C;Superfamily: Parasporal crystal protein

C; Keywords:	delta-endotoxi	toxin		;	
Alignment Scores: Pred. No.: Score: Percent Similarity: Best Local Similarit; Query Match: DB:	cores: ilarity: Similarity:	2.85e-36 672.00 43.24% 27.55% 17.06%	Length: Matches: Conservative: Mismatches: Indels: Gaps:	1160 216 1123 1128 29	
US-10-782-570	-1 (1-223	5) x I40589 (1	-1160)		
& 8	1 GTGAATCA :::::: 1 MetSerPro	AAATAATAATGAA OASNASNGINASNGIV	.TATGAGATTATCGAT TyrGluileileAsp	GTGAATCAAAATAATAATGAATATGAGATTATCGATTCAAAGAATTTATCTTATCCT	20
\$ E	61 TCTAACAGAAATATTG ::: ::: 21 SeragnagnSerlle	AAATATTGATCATTCT	AGATACCCTTACACA 	TCTAACAGAAATATTGATCATTCTAGATACCCTTACACAAATAATCCAAATCAACCATTA	120
г		AAATTACAAAGAGTGG	CTCAATATGTGTCAAC	CADADACACADATTACADAGAGTGGCTCADTATGTGTCADGGGDATACACADTATGGT	177
00 38		casniyriysaspiyi Gagacarrrgcragi	ьешувметтигсти: Сстдатасааттдст	serinrasnalagiubeuser scagnraggaggracrafr	57
			 i		75
		TACTCTGTTAGCCGGT	ATAGGTGGGCTCACT	GIATCCGGIACTCTGTIAGCCGGIAIAGGIGGGCTCACTTCTAIAICCGGACCGAIAGGA	297
Dp 40	76 Ilevalse	rThrileileSerGiy	LeuGly	iléPro	87
23 B	298 ATAATAGG	TGCTATAATAATATCT ::: yGluValPheSerIle	TTTGGTACCCTAATCJ ::: LeuGlySerLeuIle(ATAATAGGGGCTATAATAATAATATTTTGGTACCCTAATCACTGTCTTTTGGCCCGGGGA :::::: ::: ::: ValleuGlyGluValPheSerIleLeuGlySerLeuIleGlyLeuLeuTrpProSerAsn	357 107
Qy 35	358 GAACAAGAC	CAAAACAGTATGGACA :	CAATTTATTAAAATG	GAACAAGACAAAACAGTATGGACACAATTTATAAAATGGGAGAAATTTTTGTTGATACA	417
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		mapoervarargoer	AlgararieAraabp	Jenyrananaerurgirenta	n t
67 Bb 14	478 TTACAAAG :::::: 146 ValGluTy:	CTATAATACAGCATTA TyrGlnAenAlaLeu	GATGATTGGAGAAAA -:: GluABpTrpArglyB	TTACAAAGCTATAATACAGCATTAGATGATTAGAAAATTAAAAAGACTACGT :::::::	537
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. 6		ACCTATTTATGCGCA	AGCTGCTAATTTTCAT	TTAAATTTATTACAACAAGGT	
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0y 7.1	718 GCTGAATT	GGCTGATGAATGGAAT	GCAGATATACATCCT	GCTGBATTGGCTGATGGAATGCAGATATACATCCTTCACAAATTGAACCTAATGCT	777
Db 21	ß	 GlnIleTyrGlyLysGluTrpGly	::: /TyrProGln-	31n	225
7.	778 GGAACAIC	AGATGACTATTATAA	ACTTTTAAAAGAAAAT	GGAACATCAGATGACTATTATAAACTTTTAAAAGAAAATATACCTAAAATATAGTAACTAT	837
Db 22	w	eAspleuPheTyrLys	GluGlnValSerTyr	AsnAspileAspLeuPheTyrLysGluGlnValSerTyrThrAlaArgTyrSerAspHis	245
Oy 831	on v	TACCTATAGAGAAGG TTTTYTABDA	ACTAAATAAACTTCGA	TGTGCAAATACCTATAGAGAAGGACTAAAAATAAACTTCGAAAGGAACCTAATATGAGATGG 	897
		TAATGATTATCGAAG	TATATGACTATTACT	AGIATATTTAATGATTATGGAAGATATATAGACTATTACTGTATTAGATACTATCGCTCAA	957

	259 GlyThrAsnThrGluSerTrDeuArgTyTHisGlnPheArgArgGluMetThrTeuVal 278 937 GTATTAGATACTGCCCAATTTTCTTTTTAGATATAAGAGATACAAAGAGTTCAATA 996 198 ValLeuAspValValAlaLeuPheProTyTTyTASpValArgLeuTyTPTOThr 296 997 GGAGAATAGGTGGCATTAAACTGAACTTACAAGAGAAATTTATACAACTGAAATAAT 1056 1997 GGAGAATAGGTGGCATTAAACTGAACTTACAAGAGAAATTTATACAACTGAAATAAT 1056 1997 GGAGAATAGGTGGCATTAAACTGAACTTACAAGAGAAATTTATACAACTGAAATAAT 1101 11057 TTTGAC
4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8
Db 587 ArgSerProGludanProAlaThrTySerAlaSerIleAlaTyThrAssThrMetSer 606 (V) 1939 ACTTTTCTGGTACAATTATAATAATTACAATGGGGAATTTGGGTATTT 1938 ::: :::	Marches 1157

us-10-782-570-1.rpr

Page 13

a	393 IleThrThrArgAlaThrIleAenProGlyValAspGlyThrAsnArgIle 410
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S 8	1201 GANAGANCAGGICCACCCACCCACAGANACIITAAIACAIITGAAICCIAIAAAGIIICA 1320 411GluseThralayalAspPhArgSerlaLeu1961y 423
ò	AITGTAACTGATAGACAAGTAACTCCCTACCTTTTCCTAACATATACTTTACAATT
qq	424 IleTyr 425
<u>ک</u> ۾	1381
È	GGGAATTTATCTAATGATAAAAAAACAACTGATTTTCAATTTCCTGTAAAAAAGACTGT
q	
È	1501 AAACCAATTATTAATCCAAATTGTTTACCAAGCTATAATAGTTATAGT 1548
qo	450 ArgAspLeuTyrAspThrAsnAspGluLeuProProAspGluSerThrGlySerSerThr 469
දු පු	1549 CATAITTTATCCCAGTTTTCTTTATTTAATTTTCCTATAAAATTGGATTAGGCTAAAT 1608
È	1609 ATATTATATACAGGTGCATTAGGATGGACACACAGTAGTGTTAATAGAAAT 1659
DP CD	 IlealaasnalaGlySerValProThrTyrValTrpThrArgArgAsgValAspLeuAsn
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QQ	
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Dp	548 ThrAsnGlyThrPheGlyThrLeuArgValThrValAsnSerProLeuThrGlnGln 566
<u>ک</u> ج	1831 TATTACATTAGACTTCGATACGCTACAAATGGTGCTGGAAATACTCTTCCTAATATATCT 1890
} }	
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È	1948 GGTACAAATTATAATAATATTACAATACGGAGATTTTGGGTATTTTCCAATTTTCCAAGTACA 2007
qq	601ArgGlyGlnGluLeuThrTyrGluSerPhePheThrArgGluPheThr 616
ਨੇ ਨ	2008 GTAACATTACTTTAAAATCGAAACATTACATTTAAATCGTGCAGATGTATCAAAT 2067
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· 음 중	635 ThrValAsnAlaGluGlyValSerThrGlyGluTyrTyrIleAspArglleGluIle 654
ò	2098 ATACCAATTACTTCCTCTGTACGCCAAAATAGAGAAAAAAAA
· 8	::: ::: ValProvalAsnProAlaArgGluAlaGluGluAspLeuGluAlaAlaLys
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Paragporal crystal protein cry3Aal - Bacillus thuringiensis
N;Alternate names: coleopteran-specific insect control protein; crystal protein cryC; de
C;Species Bacillus thuringiensis
C;Date: 19-Nov-1988 #text change 05-Oct-2004
C;Accession: A27323; A26853; A2987; A28407; S60781; I39812; I39813
R;Herrnatdt, C.; Gilroy, T.B.; Sobleski, D.A.; Bennett, B.D.; Gaertner, F.H.
A;Title: Nucleotide sequence and deduced amino acid sequence of a coleopteran-active del
A;Reference number: A27323; MUID:88112860; PMID:2828180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: UNIPROT:Q986N9; UNIPARC:UPI00000AEBDC; GB:M22472; NID:g142733; PIDN: A;Experimental source: strain San Diego
R;Hoefte, H.; Seurinck, J.; Van Houtven, A.; Vaeck, M.
Nucleic Acids Res. 15, 7183, 1987
A;Title: Nucleotide sequence of a gene encoding an insecticidal protein of Bacillus thur A;Reference number: A26853; MUID:88015559; PMID:3658680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Experimental source: var. tenebrionis
R;Sekar, V.; Thompson, D.V.; Maroney, M.J.; Bookland, R.G.; Adang, M.J.
Proc. Natl. Acad. Sci. U.S.A. 84, 7036-7040, 1987
A;Itile: Molecular cloning and characterization of the insecticidal crystal protein gene
A;Reference number: A28407
A;Accession: A28407
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A;Residues: 9-652 <8EK>
A;Cross-references: UNIPARC:UP1000002B8CD
A;Experimental source: var. Tenabrionis
R;Adams, L.F.; Mathewes, S.; O'Hara, P.; Petersen, A.; Guertler, H.
Mol. Microbiol. 14, 381-389, 1994
A;Title: Elucidation of the mechanism of CryIIIA overproduction in a mutagenized strain
A;Reference number: S60781; MUID:95131759; PMID:7830581
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A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 9-652 <ADA>
A;Cross-references: UNIPARC:UPIO0002B8CD; EMBL:U10985; NID:g506182; PIDN:AAC43266.1; PI
A;Experimental source: var. tenebrionis strain NB176, a mutant of strain NB125
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Wu, S.J.; Dean, D.H.
J. Mol. Biol. 255, 628-640, 1996
A;Title: Punctional significance of loops in the receptor binding domain of Bacillus thu A;Reference number: 862317; MUID:96163559; PMID:8568902
A;Contents: annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ribonovan, W.P.; Gonzalez, J.M.
Mol. Gen. Genet. 214, 365-372, 1988
Aiftle: Isolation and characterization of EG2158, a new strain of Bacillus thuringiens:
A;Reference number: 139812; MUID:89112139; PMID:3146015
A;Accession: 139812
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A,Gross-references: UNIPARC:UP1000002B8CD; GB:M37207; NID:g142735; PIDN:AAA50255.1; PID
A,Experimental source: strain EG2158
R;Teixeira De Souza, M.; Lecadet, M.M.; Lereclus, D.
J. Bacteriol. 175, 2952-2260, 1993
A,Title: Pull expression of the cryIIIA toxin gene of Bacillus thuringiensis requires a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                              1069 ACTTACCTTGAAATTCAACCCAATCTCGCTATAATGGAATATAAATTTAACACGTTCAGGG 1128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      428 ThrLysValGluPheSerGlnTyrAsnAspGlnThrAspGluAlaSerThrGlnThrTyr 447
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---AlaGluPheTyrLysArgGlnLeuLysLeuThrGlnGluTyr
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ThrasphisCysVallysTrpTyrasnValGlyLeuAspLysEuArgGlySerSerTyr
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LysSerSerGluProValGlnAsnLeuGluPheAsnGlyGluLysValTyrArgAlaVal
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A;Reference number: 139813; MUID:93259939; PMID:8491716
A;Accession: 139813
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Nolecule type: DNA
A;Residues: 9-58 <REZ>
A;Cross-references: UNIPARC:UPI000000007B; GB:L03393; NID:g304150; PIDN:AAA22350.1; |
C;Gene:tos:
A;Gene: crylIIA
C;Superfamily: Parasporal crystal protein
C;Keywords: delta-endotoxin
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AspPro-----TrpLysAlaPheMetGluGlnValGluAlaLeuMetAspGln 127
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-----GlyalaLeuValSerPheTyrThrAsnPheLeuAsnThr1leTrpProSerGlu 111
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ProThrAsn------HisValGInTyrProLeuAlaGluThrProAsnProThr 44
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---AsnThrGluAlaLeuAspSerSerThrThrLysAspVallleGlnLysGlyIleSer 79
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ValGluAgpTyrValSerAlaLeuSerSerTrpGlnLys-------
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Matches:
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301 ATAGGTGCTATAATAATATCTTTTGGTACCCTAATCACTGTCTTTTGGCCCGGGGAGAA 360		361 CAAGACAAAACAGTATGGACACAATTTATTAAAATGGGAGAAATTTTTGTTGATACACCG 420	90 AspGlnTrpGlullePheLeuGluHisValGluGlnLeuileAsnGlnGln	421 TTAACAGAAAGGATAAACAGGTTAAGAAAGGATTTAGAAGGATTTAGACAATATTA 480 ::: ::: 107 IleThrOllagnalaArgaganThrAlaLeualaArgLeuGlnG-YLeuGlyAspSerPhe 126	481 CAAAGCTATAATACAGCATTAGATGATTGGAGAAAATTAAAAAGACTACAAGGCTCCTGGA 540	::::: ::: ::: ::: 127 ArgAlaTyrGlnGlnSerLeuGluAspTrpLeuGluAsnArgAspAsp 142	541 TTACCACCATCACCATTACAACAAGCTGCCTTGACTCTTAAAATACGATTTGAGAAT	143 AlaArgThrArgSerValLeuTyrThrGlnTyrIleAlaLeuGluLeu 158 601 GTTCACAATGATTTTATTCGAGAAATACCTGGTTTCCAACTTGAAACTTATAAAACGCTA 660	::: 159ABPPheLeuAsnAlaMetProLeuPheAlalleArgAsnGlnGluValPro 175	661 TTACTACCTATTTATGGGCAAGCTGGTAATTTTCATTTAAATTTATAAAAGTGGT 720 :::	721 GAATTGGCTGATGAATGCAGATATACATCCTTCACAAATTGAACCTAATGCTGGA	196 LeuPheGlySerĠi 781 ACATCAGATGAC	:::	832 AACTATTGGGAAATACCTATAGAGGAGTAAATAAACTTCGAAAGGAACCTAATATG	224 AspTyrCysValGluTrpTyrAsnThrGlyLeuAsnSerLeuArgGlyThrAsnAlaAla	892 AGAIGGAGIATATITAANGAITATCGAAGAIATATATGACTATIACIGIATIAGAIACIAIT 951	952 GCTCAATTTTCTTTTATGATATAAGGATACAAAGATTCAATAGGAAGAATAGGTGGC	264 AlaLeuPheProSerTyrAspThrArgThrTyrProlleAsn 277	278 ThrSerAlaGinLeuThrArgGluValTyrThrAspAlaileGlyAlaThrGlyValAsn	1057 TITGACCGTCTTACTTACCTTGAAATTCAACCGAATCTCGCTATAATGAATATAAT		318 AlaileArgSerProHisteuLeuAspPheLeuGluGlnLeuThrllePheSerAla	1165	337 SerSerArgTrpSerAenThrArgHisMetThrTyrTrpArgGlyHisThrIleGlnSer	1192 CGTTIAGTIGGGAATICGTAATAGATCTAATTATGATGACGACGACGAATT 1231 	1252 ATATATGGAGAAAGAACAGGTCCACCACAACAAAAACTTTAATACCA 1299
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	OY 1828 TCTTATTACATTAGACTTCGATAGGCTACAAATGGTGCTGGAAATACTCTTCCTAATATA 1887	Db 568 LysTyrArgAlaArgIleHisTyrAlaSerThrSerGlnIle 581	1888 TCTCTTACAATACCAGGAGTAATAGGAATACCACCTCAACGACTCAACAACACTTTTTCT	DD 582 ThrPheThrLeuSerLeuAapGlyAlaProPheAshGlnTyrTyrPhe 597 Qy 1948 GGTACAAATTATAATAATTTACAATACGGAGATTTTGGGTATTTCCAATT 1998		Oy 1999 CCAAGTACAGTAACATTACCTTTAAATCGAAACATACCATTTAATATTTAATCGTGCAGAT 2058	618	<pre>Qy 2059 GTATCAAATTTAATCATTGATAAAATTGAATTTATACCAATT 2106 ::: ::: ::: :: Db 637 AlaGlyAspLy8ValTyrIleAspLysIleGluPheIleProVal 651</pre>	RESULT 11	o. thur	.juate. vsep-1590 #Bequence_revision vsep-1990 #text_cnange vs-oct-2004 C;Accession: S00873 R;Brizzard, B.L.; Whiteley, H.R.	Nucleic Acids Res. 16, 2723-2724, 1988 Ayfitle: Nucleotide sequence of an additional crystal protein gene cloned from Bacillus AyReference number: 800873; WUID:88223216; PMID:3362680	A;Accession: S00873 A;Molecule type: DNA	A;ReBidues: 1-1228 <bri> A;Cross-references: UNIPROT:P05517; UNIPARC:UP10000126BDC; EMBL:X06711; NID:g40264; PIDN C;Genetics:</bri>		C;Superfamily: Pàrasporal crystal protein C;Keywords: delta-endotoxin	4.87e-32 Length: 607.00 Matches:	ative: hes:	2 2 1/ (1-00000 - (1-00000) (1-10000)	OS-10-101-510-1 (T-2235) A SOUGES (T-1226) QY GGAATGAAATAATAATAATGAATATGAGATTATCGATTCAAAGAATTTATCTTATCCT 60	:::	61 TCTAACAGAAATATTGATCATTCTAGATACCTTACACAAATAATCCAAATCAACCATTA	Db 16 SerAsnHisSerAlaGinMetAspLeuLeuPro	27AspalaArg1leGluAspSerLeuCys1lealaGluGlyAsn	Oy 181 AATTTCGAGACATTTGCTAGTGCTGATACAATTGCTGCAGGTAGTGGTACTATTGTA 240	241 TCCGGTACTCTGTTAGCCGGTATAGGTGGGCTCACTTCTATATCCGGACCGATAGGAATA

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1420 AAATTAACATATTCAGCTGGGGGAATTTATCTAATGATAAAAAAACAACTGATTTTCAA 1479
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TTTGAATCCTATAAAGTTTCAATTGTAACTGATAGACAAGTAACTCCTACTTCCCCTTTT 1359
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ThrGluSerTyrAlaGlyValLeuLeuTrpGlylleTyrLeuGluProlleHisGlyVal
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432 GlnProTyrGluSerProGlyLeuGlnLeuLyBABpSerGluThrGluLeuProProGlu
                                                                                                                                                                                                                                                                                                  543 ValAsnGlyPro---LeuThrGlnArgTyrArglleGlyPheArgTyrAlaSerThrVal
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Cyaccesion: 139815
Rights: Screening by Williams, R.; Hedges, R.J.
Appl. Environ. Microbiol. 59, 1683-1687, 1953
A;Title: Screening by polymeraee chain reaction of Bacillus thuringlensis serotypes for lensis subsp. Kurstakt.
A;Reference number: 139815; MUID:93298009; PMID:8517758
A;Accession: 139815
A;Accession: 139815
A;Accession: Dreliminary; translated from GB/EMBL/DDBJ
A;Residues: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-719 cRES>
C;Genetics:
A;Cross-references: UNIPROT:Q45752; UNIPARC:UPI0000036008; GB:M98544; NID:g142767; PIDN: C;Superfamily: Parasporal crystal protein
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127 AspLeuLysGlyLeuGlyAspAlaLeuAlaValTyrHisAspSerLeuGluSerTrpVal 146
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70 IleLeuGlyThrLeuGlyValProPheAlaGlyGlnValAlaSerLeuTyrSerPheIle 89
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insecticidal protein cryV - Bacillus thuringiensis
C;Species: Bacillus thuringiensis
C;Date: 19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change 05-Oct-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         43 AAGAATTTATCTTATCCTTCTAACAGAAATATTGATCAT---TCTAGATACCCTTACACA
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Matches:
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588.50
40.23%
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Query Match:
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Pred. No.:
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insecticidal protein cryVI - Bacillus thuringiensis
C;Species: Bacillus thuringiensis
C;Date: 19-JU1-1996 #sequence_revision 19-JU1-1996 #text_change 05-Oct-2004
C;Accession: 139814
R;Shin, B.S.; Park, S.H.; Choi, S.K.; Koo, B.T.; Lee, S.T.; Kim, J.I.
Appl. Environ. Microbiol. 61, 2402-2407, 1995
A;Title: Distribution of cryV-type insecticidal protein genes in Bacillus thuringiensis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Cross-references: UNIPARC: UPI0000036009; GB: L36338; NID: 9540281; PIDN: AAC3699.1; PID:
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                                                                                                                                                                                             -----AATGGTGCTGGA 1869
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                                                                                                                        -----CGTTTAGAGATTACATGTAGAACTCCTAATTCTACACAATCTTATTACATT 1839
505 AsnSerIleThrGlnIleProLeuValLysAlaPheAsnLeuSerSerGlyAlaAlaVal 524
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---LeudapValGlnSerThrPheThrIleGlyAlaTrpAsnPheSerSerGlyAsnGlu 632
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------PheGluLysAlaGlnGluLysValThrAlaLeuPheThrSerThrAsnPro 669
                                                                          2050 CGTGCAGATGTATCAAATTCAATTTTAATC-----
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                                                     2194 AATACTTTAAATATAGAAGCCACAAACTATGATATTGAT 2232
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A;Accession: 139814
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A;Molecule type: DNA
A;Residues: 1-719 <RES>
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C;Genetics

A;Gene: cryV1 C;Superfamily: Parasporal crystal protein

719 207 1111 294 181 Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps: 1.22e-30 585.50 40.10% 26.10% Percent Similarity: Best Local Similarity: Query Match: DB: Alignment Scores: Pred. No.:

US-10-782-570-1 (1-2235) x I39814 (1-719)

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43 AAGAATTTAICCTTCTAACAGAAATATTGAICAITCTAGATACCCTTACACA 99		TGCA	46SerGluTyrGluAenValGluProPheValSerAlaSerThr1leGln 61 220 GTTAGTGCAGGTACTATTGTATCCGGTACTCTGTTAGCCGGTATAGGTGGGCTCACTTCT 279		280 ATATCCGGACCGATAGGATAATAGGTGCTATAATAATATTTTTTTGGTACCCTA 333	334 ATCACTGTCTTTTGGCCCGGGGAGAACAAAAAACAGTATGGACACAATTTATTAAA 393	LeuGlyGluLeuTrpProLysGlyLysAanGlnTrpGluIlePheMetGlu	394 ATGGGAGAAATTTTTGTTGATACACCGTTAACAGAAAGCATAAAAGATAAGTTACAA 453 	454 ACTITAGAAGGATITAGACAAATATTACAAAGCTATAATACAGCATTAGATGATTGG 510	AGAAAATTAAAAAGACTACAAGGTTCCTGGATTACCACCATCATCAGCATTACAA	:::::: 147 GlyAsnArgAsnAsnThrArgAlaArgServalvalLys 159	CAAGCTGCCTTGACTCTTAAAATACGATTTGAGAATGTTCACAATGATTTTATTCGAGAA	SerGlnTyrIleAlaLeuGluLeuMet	625 ATACCTGGTTTCCAACTTGAAACTTATAAAACGCTATTACTACTATTTATGCGCAAGCT 684 :::	685 GCTAATTTTCATTTAATTTATTACAACAAGTGCTGAATTGGCTGATGGAATGCA 744	193 AlaAsnLeuHisLeuLeuLeuLeuArgAspAlaSerIlePheGlyLysGluTrpGly 211	745 GATATACATCCTTCACAAATTGAACCTAATGCTGGAACATCAGATGACTATTATAAACTT 804 ::: -::: 212LeuSerSerSerGluileSerThrPheTyrAenArg 223	805 TIBABAGBABATATACCTABATATAGTBACTATTGTGCABATACCTATAGAGAGAGTA 864	224 GlnValGluArgAlaGlyAspTyrSerTyrHisCysValLysTrpTyrSerThrGlyLeu 243	AATAAACTTCGAAACGAACCTAATATGAGATGGAGTATATTAATGATTATCGAAGATAT	244 AsnAsnLeuArgGlyThrAsnAlaGluSerTrpValArgTyrAsnGlnPheArgArgAsp 263	925 ATGACTATTACTGTATTAGATACTATCGCTCAATTTTCTTTTATGATATAAAGAGATAC 984 :::	985 AAAGAITCAAIAGGAAGAAIAGGIGGCAIIAAAACIGAACIIACAAGAGAATI 1038	284 Pro	1039 TATACAACTGAAATAAATTTTTGACCGTCTTACTTAC 1074	CTTGAAATTCAACCCAATCTCGCTATAATGGAATATAATTTAACACGTTCAGGGCTTAGA
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404 LeualaGlyLeuAsnLeuPheLeuThrGlnProValAsnGlyValProArgValAspPhe 423 ------HisTrpLysPheValThrHisProlleAlaSerAspAsnPheTyrTyrPro 440 ::: ||| ::: ||| 41 GlyTyralaGlyThrGlnLeuGlnAspSerGluAsnGluLeuProProGluAla 460 1495 GACTGTAAACCAATTATTAATCCAAATTGTTTACCAAGCTATAATAGTTATAGTCATATT 1554 ii: 461 ThrGlyGln-----------ProAsnTyrGluSerTyrSerHisArg 472 ||||||| ::: |||::: ||| 473 LeuSerHisIleGlyLeuIleSerAlaSerHisValLysAlaLeuValTyrSer----- 490 524 561 1675 AAAATAATTACAATGATCCCAGCAATCAAAGGTAACAGTCTTGATACAAACTCTAAGGTA GTAACTGATAGACAAGTAACTCCTACTTCCCCT-----TTTCCTAACATACTTT 582 IleAsnGlnGlyAsnPheSerAlaThrMet---------TTATTTTCATTTTAGATGAACTTATATTTTATACA-1180 ACGTACGGGAAT----335 1135 1324 424 491

	DD 173 LeubroSerPheAlaValSerGlyGluGluValProLeubrolletyTALaGLANAIA Qy 685 GCTAATTTCATTTAAATTTATTACAAGGGTGCTGAATGGCTGATGAATGGCAGAAGGAATGCA 193 AlaAenLeuHisLeuLeuLeuLeubrgaspalaSerIlePheGlyLygGluTrpGly Qy 745 GATATACATCCTTCACAAATTGAACCTAATGCTGGAACATCAGATGATTATAAACTT 1::	Oy 925 ATGACTATTACTGTATTAGATACTATCGCTCAATTTTCTTTTTATGATATAAAGAGATAC	1075 CTTGAAATTCAACCCAATCTCGCTATAATGGAATATA	Oy 1180 ACGTACGGAAT		OY 1375 ACANTIAATCAAATTOAACTTTATTAAATAATTCCCTAGTAATAATTAACATAATTCA 1434 124HistrpLysPheValThrHisProllealaSerAspAsnPheTyrTyrPro 440 COY 1435 GCTGGGGGGAATTTATCTAATGATAAAAAACAACTGATTTTCAATTTCCTGTAAAAAAA 1494
614LeuaspvalGlnSerThrPheThrIleGlyAlaTrpAsnPheSerSerGlyAsnGlu 632 2080ATTGATAAAATTGAATTTATACCAATTACTTCCTCTGTACGCCAAATAGAGAA 2133 5180ATTGATAAAATTTATACCAATTACTTCCTTGTACGCCAAATAGAA 2133 5181 ValTyrIleAsparglleGluPheValProValGluValThrTyrGluAlaGluTyrAsp 652 2134 AAACAAAAATTAGAAACTATCCAAAAAAAAAAAAAAAAA	PRESULT 14 S25383 parasporal crystal protein crylIal - Bacillus thuringiensis Nalternate names: delta-endotoxin; parasporal crystal protein cryv C;Alexate names: delta-endotoxin; parasporal crystal protein cryv C;Accession: S55383 C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 05-Oct-2004 C;Accession: S55383 R;Tailor, R; Tippett, J; Gibb, G; Pells, S; Pike, D; Jordan, L; Ely, S. Mol. Microbiol. 6, 1211-1217, 1992 A;Title: Identification and characterization of a novel Bacillus thuringiensis delta-end A;Accession: S25383 A;Accession: S25383 A;Accession: S25383 A;Accession: C25383 A;Accession: C25883 A	Algame: cryV C;Superfamily: Parasporal crystal protein C;Superfamily: Parasporal crystal protein C;Superfamily: Alianarity: 1.22e-30 Length: 719 Red. No.: 585.50 Matches: 207 Score: 6.10* Conservative: 111 Best Local Similarity: 26.10* Mismatches: 294 Query Match: 14.86* Indels: 181 DB: 2 Gaps: 34	US-10-782-570-1 (1-2235) x S25383 (1-719) Qy	GGGAATACACAATATGGTGATAATTTCGAGACATTTGCTAGTGCTGATACAATTGCTGCA ::::::	62Thrdlylledladlylby8 69 280 ATATCCGGACCGATAGGAATAATAGGTGCTATAATAATATCTTTTGGTACCCTA 333 281 ATATCCGGACCGATAGGAATAATAGGTGCTATAATAATATCTTTTGGTACCCTA 333 334 ATCACTGTCTTTTGGCCGCGGGGGAACAACAGAACAGTATGGACACAATTTATTAAA 393 334 ATCACTGTCTTTTTGGCCCGCGGGGAACAACAGAACAGTATGGACACAATTTATTAAA 393 336 ATCACTGTCTTTTTGGCCCGCGGGGAACAACAGAACAGTATGGACACAATTTATTAAA 393 337 ATCACTGTCTTTTTTTTTTTTTTAAA 393 338 ATCACTGTCTTTTTTTTTTTTTTTAAA 393	394 ATGGGAGAATTTTTGTTGATACACGGTTAACAGAAAGCATAAAACAGCTAAAGTTACAA 453

EMBL:X54160; NID:940279; PIDN

A;Cross-references: UNIPROT:P19415; UNIPARC:UPI00002COA3; EMBL:X54160; NID:g402*C;Superfamily: Parasporal crystal protein C;Keywords: delta-endotoxin Alignment Scores: Pred. No.: Score: Score: Score: Score: Score: Score: A1.49* Conservative: 119 Per cent Similarity: 26.549* Conservative: 119 Best Local Similarity: 26.549* Usery Match: Cousty Match: C		Db 16 SerAenProLysGluIleIleLeuGlyGluGluArgLeuGluThrGlyAenThr 33 Qy 211 ATTGCTGCAGTTAGTGCAGGTACTATTGTATCCGGTACTCTGTTAGCCGGTATA 264	53	/> PRELEGIAGIALIEGIAGIALIESSENCIAAEGIIEGIAGIARIGAEGABACIAL 445 AAGTTACAAACTTTAGAAGGATTTAGACAAATATTACAAAGCTATAATACAGCATTAGAT :::	Oy 565 CAAGCTGCCTTGAATACGATTTGAAATGTTCACAATGTTTATTCAGAA 624 1127 GluGluMetArglieGlnPheAenspMetAsnSeralaLeulleThrala 143 Oy 625 ATACCTGCTTTCCAACTTATAAAACGCTATTACTACCTATTTATGCGCAAGCT 684 Db 144 IleProLeuPheArgValGlnAenTyrGluValAlaLeuLeuSerValTyrValGlnAala 163	
Db 441 GlyTyralaGlyThrGlnLeuGlnAspSerGluAsnGluLeuFroProGluAla 460 Qy 1495 GACTGTAAACCAATTATTAATCCAAATTGTTTACCAAGCTATAATAGTCATATT 1554	Qy 1675 AAAATAATTACAATGATCCCAGCAATCAAAGGTAACAGTCTTGATACAACTCTAAGGTA 1734 Column	Db 525 ValargGlyProGlyPheThrGlyGlyAspIleLeuArgArgThrAshThrGlyThrPhe 544 Qy 1789CGTTTAGAGATTACATGTAGAACTCCTAATTCTACACAATCTTATTACATT 1839	562 ATGILGARGINETH SECONDARY SECTION S	592	Oy 2080ATTGATAAATTGAATTTATACCAATTACTTCCTCTGTACGCCAAATAGAGAA 2133	SULT 15 SULT 15 SULT 15 SULT 15 Taggoral crystal protein crylDal - Bacillus thuring; Alternate names: parasporal crystal protein crylDal - Bacillus thuring; Alternate names: parasporal crystal protein crylD Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #tc Accession: S1146 Hoffte, H.; Soetaert, P.; Jansens, S.; Peferoen, M. Cloic Acids Rea. 18, 5545, 1990 Title: Nucleotide sequence and deduced amino acid se Reference number: S11446; MUID:91016642; PMID:22167; Accession: S1446 Status: preliminary Molecule type: DNA Residues: 1-1165 < HOS>

À.	985 AAAGATTCAATAGGAAGAATAGGTGGCATTAAAACTGAACTTACAAGAGAAATTTATACA 1044	
ą	255 ProlleGlnThrAla 267	
À	1045 ACTGAAATATTTGACCGTCTTACTTACCTTGAAATTCAACCCAATCTCGCT 1098	
ą	268 LeuAspLeuProPheIleAsnGluAsnLeuSerProAlaAlaSerTyrProThrPheSer 287	
≿ °≅	1099 ATAATGGAATATAATTTAACACGTTCAGGGCTTAGATTTTTTATTTTTTTT	
: ≿	ATATTTTATACAAAAAATGAAACGTACGGGAATCGTTTAGTTGGTATTGCGAATCGTAAT	
ą	307 ThrlleTyrThrAspSer 312	
⋩	1219 AGATCTACTTATGCTACGACAGGAACTGAAATTATATATGGAGAAAGAA	
ą	ii:	
à	1279 ACAACAAAAACTTTAATACCATTTGAATCCTATAAAGTTTCAATTGTAACTGATAGACAA 1338	
ą	331 ThrThrThrAsnLeuileArgSerProLeuTyrGlyArgGluGlyAsnThrGluArgPro 350	
à	1339 GTAACTCCTACT TCCCCTTTTCCTAACATAACTTTACAATTAATCAAATTGAACTT 1395	
q	351 ValThrileThrAlaSerProSerValProllePheArgThrLeuSerTyrIleThrGly 370	
à	1396 TATTTAAATAATTCACCTAGTAATAAATTAACATATTCAGCTGGGGGGAATTTATCTAAT 1455	
q	371 LeuAspAsnSerAsnProValAlaGlyIle	
à	1456 GATAAAAAAACAACTGATTTTCAATTTTCCTGTAAAAAAGACTGTAAA 1503	
qo	381GluGlyValGluPheGlnAsnThrIleSerArgSerIleTyrArgLysSerGly 398	
à	1504 CCAATTATTAATCCAAATTGTTTACCAAGCTATAATAGT	
qo	::: :: :::: :::::	
à	TATAGECATATITIATCCCAGITITETITATITIAATTATECTATAAAATTGGATTAGGCG	
අ	419 TyrSerHisArgLeuCysHisAlaThrPheLeuGluArgIleSerGlyProArgIleAla 438	
ጵ ብ	1603 CTAAATATATATACAGGTGCATTAGGACACACACAGTAGTGTTAATAGAATAAT 1662 	
À	1663 GCAATATCAGATAAAATAATTACAATGCCAGCAATCAAAGGTAACAGTCTTGATACA 1722	
q	::: ::: ::: ::: ::: 454 GluvalSerProSerArglleThrGln1leProTrpValLysAlaHisThrLeuAlaSer 473	
à	1723 AACTCTAAGGTAATTGAAGGACCTGGTCATACAGGAAACTTGGTTTATTTA	
д	474 GlyalaservalileLysGlyProdlyPheThrGlyGlyapIleLeuThrArgAsnser 493	
à	1783 CAAGGG	
QQ Q	494 MetdiyGluLeuGlyThrLeuArgvalThrPheThrGlyArgLeuProGin 510	
È	1828 TCTTATTACATTACACTTCCATACGCTACAAATGGTGCTGGA 1869	
g G	511 SertyrtyrileArgPheArgTyrAlaSerValAlaAsnArgSerGlyThrPheArgTyr 530	
हें ह	AATACTCTTACTAATATATACTCTTACAATACCAGGGGTAATAGGAATACCACCTCAACGA	
9	551 SerginkiokroseriyidayileserknekrobyBinimecABpAladiydlukrobeu 550	
à.	1930 CTCAACAACACTTTTTCTGGTACAAATTATAATATTACAATACGGAGATTTTGGGTAT 1989	
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ò	1990	1990 TICCAAITICCAAGTACAGTAACAITACCTITAAAICGAAACAIACCAITITATATI 2049	2049
ą	563		267
ò	2050	2050 CGTGCAGATGTATCAAATTCTAAATCATTGATAAAATTGAA 2094	2094
ą	568	568 ArgAlaGlnGluGluPheAspLeuTyrIleGlnSerGlyValTyrIleAspArglleGlu 587	587
ò	2095	2095 TTTATACCAATTACTTCCTCTGTACGCCAAAATAGAGAAAAAAAA	2154
qq	588	588 PhelleProValThrAlaThrPheGluAlaGluTyrAspLeuGluArgAla 604	604
ò	2155	2155 CAAACAAAATAATACATTTTCACAAATCATACAAAAAAAA	2214
qa	605	605 GlnLygValValAsnAlaLeuPheThrSerThrAsnGlnLeuGlyLeuLygThrAspVal 624	624
ò	2215	2215 ACAAACTATGATATTGAT 2232	
g G	625	ThraspTyrHisIleAsp 630	

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Ward B.S., Ellar D.J.;
"Nucleotide sequence of a Bacillus thuringiensis var. israelensis gene
encoding a 130 kDa delta-endotoxin.";
Nucleic Acids Res. 15:7195-7195(1987).
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-1- PUNCTION: Promotes colloidosmotic lysis by binding to the midgut epithelial cells of insects.
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01-AUG-1990 (Rel. 15, Last sequence update)
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Pesticidial crystal protein cry4Aa (Insecticidal delta-endotoxin CryIvA(a)) (Crystaline entomocidal protoxin) (135 kDa crystal
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Bacillus thuringiensis subsp. israelensis.
Plasmid 72 Kb.
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   SerThrTyrileSerAsnAlaAsnLysIleLeuAsnArgSerPheAsnValIleSerThr 150
                                                                                                                                      -----GlyValGlnSerGluLeuThrArgGluIleTyrGlnVal----LeuAsnPheGlu
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                                         TATAATACAGCATTAGATGATTGGAGAAAATTAAAAAGACTACAAGCTCCTGGATTACCA
                                                                             151 TyrHisAsnHisLeuLysThrTrpGlu------AsnAsnProAsnProGln
                                                                                                                  CCATCATCAGCATTACAACAAGCTGCCTTGACTCTTAAAATACGATTTGAGAATGTTCAC
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                                                                                                                                                                                        s Swiss-Prot entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - Buropean Bioinformatics Institute. There are no restrictions on its as long as its content is in no way modified and this statement is not
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                                                                                           MISCELLANBOUS: Diverse amino acid mutations in sequence block 667-676 have no direct effect on the insecticidal activity but alter the structural stability of the toxin protein molecule. SIMILARITY: Belongs to the delta endotoxin family.
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                                                     MISCELLANEOUS: Toxic segment of the protein is located in the N-terminus.
DEVELOPMENTAL STAGE: The crystal protein is produced during sporulation and is accumulated both as an inclusion and as part
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -> V (in Ref. 2).
-> I (in Ref. 2).
-> G (in Ref. 2).
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EMBL; Y00423; CAA68485.1; -; Genomic_DNA.
PIR; A26858 A26688.

PIR; 19870; 138970.
InterPro; IPR001178; Endotoxin.
InterPro; IPR00538; endotoxin.C.
InterPro; IPR00538; endotoxin.N.
Pfam; PP03944; Endotoxin.M; 1.
Pfam; PP0355; Endotoxin.M; 1.
Pfam; PP0355; Endotoxin.M; 1.
Plasmid; Dp0145; Endotoxin.M; 1.
Plasmid; Dp0141; Endotoxin.N; 1.
Plasmid; Dp0141; 1052 T -> I (in Ref. CONFLICT 1109 1109 R -> G (in Ref. CONFLICT 1127 1127 C -> W (in Ref. CONFLICT 1127 C -> W (in R
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|TyAspLeu11e-----AspPheLysAspHisPheLysIleThrCysGlnHisSerAsn
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                                                                                                       511 AlaThrTyrLys------ThrGlnValTyrThrPheAla-----TrpThr
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|Hi8SerSerValAgpProLy8AgnThrIleTyrThrHi8LeuThrThrGlnIleProAla
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MEDLINE=22235415; PubMed=12324359;
DOI=10.1128/AEM.68.10.5082-5095.2002;
DOI=10.1128/AEM.68.10.5082-5095.2002;
Berry C., O'Niel S., Ben-Dov R., Jones A.P., Murphy L., Quail M.A., Harris D., Zaritsky A., Parkhill J.;
"Complete sequence and organisation of pBtoxis, the toxin-coding plasmid of Bacillus thuringiensis subsp. israelensis.";
Appl. Environ. Microbiol. 68:5082-5095(2002).
EMBL, AL731825; CAD301481; -; Genomic DNA.
SEQUENCE 1180 AA; 134538 MW; GFB5E6979DACAD3B CRC64;
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10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
Pesticidial crystal protein cry4AA.
Name=cry4AA; Symonyms=cry1VA(A), isrH4, pBt110;
Bacillus thuringiensis (subsp. israelensis).
Bacillus cereus group.
Bacillus cereus group.
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112 AsnThr---TrpSerAspPhelleThrGlnThrLysAsnIlelleLysLysGlulleAla 130
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AsnLysAsnGluTyrGluThrLeuAsnAlaSerGlnLysLysLysLeuAsnIleSerAsnAsn
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|GluThrPheIleAspSer-----GlyGluLeuSerAlaTyrThrIleValValGly
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283
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Length:
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5.16e-70
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Q9FDCO;
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375 ThrProAsnAsnPhePhe---ThrSerH1sTyrAsnMetPheH1sTyrThrLeuAspAsn
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LysTyrLeuAsnAspTyrAsnAsnIleSerLysMetAspPhePheIleThrAsnGlyThr
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------AlaPheAlaSerPheValAsnPro-------GlyValValLeuIle 60
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Bacillus thuringlensis (subsp. finitimus).
Bacillus thrmicutes; Bacillales; Bacillaceae; Bacillus;
Bacillus cereus group.
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Parasporal inclusion protein Cry.
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Submitted (JUL-2000) to the EMBL/GenBank/DDBJ dat
EMBL; AF285775; AAG00235.1; -; Genomic_DNA.
HSSP; O06117; LJIG.
GO; GO:001678; Pihydrolase activity; IEA.
GO; GO:000552; Pieferse response; IEA.
GO; GO:000552; Pieferse response; IEA.
GO; GO:0004055; Pieferse response; IEA.
GO; GO:0004055; Pieferse response; IEA.
InterPro; IPR00178; Endoroxin.
InterPro; IPR005639; endotoxin.C.
InterPro; IPR005639; endotoxin.N.
Pfam; PF03944; Endotoxin.N.
Pfam; PF03944; Endotoxin.N.
Pfam; PF03945; Endotoxin.N.;
Pfam; PF03945; Endotoxin.N.;
Pfam; PF03945; Endotoxin.N.;
SEQUENCE 1128 AA; 127450 MW; 61B0DC9454BDF0E8
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us-10-782-570-1.rup

	Oy 1447 TTA	::: Db 414 Val	Qy 1498 TGT	Db 427	Oy 1552 AT	441		1612	Db 461 Ile	Qy 1672 GAT	Db 479 Glu	Qy 1732 GTA	Db 498 Val	Qy 1792 TT	Db 516 Cye	Oy 1852 GCT		Qy 1912 GGA	Db 555	Oy 1966	Db 569 Ile	Ov 2017 CCI	583	2071		2131		979	N	Db 646	RESULT 4 C28AA_BACTF		DT 16-0CT-2001 DT 16-0CT-2001	DE Pesticidial			OC Baccella; Fi
81 TrnSerg]nPheMetivsHjag]vg]nAanLenjenBang]nThr1]eSerThr2]aVa] 100		AAACAGTIACAAACTTTAGAAGATTTAGACAATATTATTACAAAGCTATAATACA		GCATTAGATGATTGGAGAAATTAAAAAGACTACAAGCTCCTGGAT	121 AlaPheAshAspIrpLysArgAshProSerAla 131	556 GCATTACAACAAGCTTGACTCTTAAAATACGATTTGAGAATGTTCACAATGATTTT 615	132AsnThrAlaArgLeuValSerGlnArgPheGluAsnAlaHisPheAsnPhe 148	616 AFTCGAGAAATACCTGGTTTCCAACTTGAAACTTATAAAACGCTATTACTACTATTTAT 675	valSerAsnMetProGlnLeuGlnLeuGrachtrytAspThrLeuLeuLeuSerCvsTvr	R RATHER CATHATA STATEMENT & REPORT OF RATHAR RATHAR RATHAR RATHARAN RATHAR			Togethic-Meanaran Control Charite Annual Control Contr	Trpashataaspernkronisserkrometleulyssersergiyinrtyr	/90 INTARABLITITARABLARANIATARCITATARA 833	17 Abbotuneuvat 17 I Tectunyat 17 I Technil 3 I Cybrill 19 I II I I I I I I I I I I I I I I I I	GAAGGACTAAATAAACTITCGAAACGAACCTAATATGAGATGGAGTATATTTAATGATTATTATTAATTATT	LysGiyLeuasnhisLeuLysGiuSerGiuLyslieinrirpaspalalyrasninriyr	CGAAGATATATGACTATTACTGATTAGATACTATCGCTCAATTTTCTTTTTAGATATATAT	Argargelumetinzbeullevalbeukappeuvalalainrrneriornelyraspile 205	AAGAGATACAAAGATTCAATAGGAAGAATAGGTGGCATTAAAACTGAACTTACAAGAGAA ::: :::	266 ArgArgPheProArgGlyValGluLeuGluLeuThrArgGlu 279	1036 ATTTATACAACT1059	280 VallyrThrSerLeuAspProProGlyLeuAsnAlaGlyProIleProGluileAspPhe 299	1060 GACCGTCTTACCTTGAAATTCAACCCAATCTCGCTATAATGGAATATAATTTAACA 1119	300SerTyrLeuGluAspHisLeuThr 307	1120 CGTTCAGGGCTTAGATTATTTTTAGATGAACTTATATTTTATACAAAAATGAA 1179		1180 ACCTACGGGAATCCTTTAGTTGGTATTGCGAATCGTAATAGATCTACTTATGCTACGACA 1239	::: 327	-ATATATGGAGA	::: 343 GlyasnGlnPhePheThrMetLysAsnIleTyrGlyAsnThrAsn 357	1285 AAAACTTTAATAÇATTTGAATCCTATAAAGTTTCAATTGTA 1326	::: :: ::: :::	1327 ACTGATAGACAAGTAACTCCTACTTCCCTAACATATACTTTACAATTAATCAA 1386	377 IleAsnArgGlyPheGlnThrIleAlaGlyIleAsnLysLeuTyrSerLeuIleGlnLys 396	1387 844722222232447
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TAAACCAATTATTAATCCAAATTGTTTACCAAGCTATAATAGT-----TATAGTCAT 1551
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coluserglugluileHisileHisLeulysArgGluAspAgTyrGluGluGlyVal 608
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snGluMetAsnLeuGluLysAlaLysLysAlaValAsnValLeuPheIleAsnAlaThr 645
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1 (Rel. 40, Last sequence update)
5 (Rel. 48, Last annotation update)
1 crystal protein cry28Aa (Insecticidal delta-endotoxin crystal) (Crystalline entomocidal protoxin) (126 kDa crystal
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huringiensis subsp. finitimus.
Firmicutes; Bacillales; Bacillaceae; Bacillus;
                        PRT; 1109 AA
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                                                                                                                                                                                          This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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|AlaPheAsnAspTrpLysArg-----AspFroSerAla 131
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|SerSerAspThiValAlavalValSerAlaGlyIleValValValGlyThrIleLeuThr 47
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LysGlulleAlaLeuAlaHisLeuAsnGlyPheLysAspValLeuThrTyrTyrGluArg
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                 MEDILINE-993301665 PubMed=10403372; DOI=10.1016/S0014-5793(99)00650-X; Wojciechowska J.A., Lewitin B., Revina L.P., Zalunin I.A., Chestukhina G.G.;
Two novel delta-endotoxin gene families cry26 and cry28 from Bacillu.
Thuringlensis ssp. finitimus.";
FEBS Lett. 453:46-48(1999).
-!- FUNCTION: Promotes colloidosmotic lysis by binding to the midgut epithelial cells of insects.
-!- FUNCTION: Promotes colloidosmotic lysis by binding to the midgut epithelial cells of insects.
-!- FUNCTION: Promotes colloidosmotic lysis by binding to the midgut epithelial cells of insects.
                                                                                                                                                MISCELLANEOUS: Toxic segment of the protein is located in the N-
                                                                                                                                                                                                                                                                                                                                                                     10C80705508F5CDA CRC64;
                                                                                                                                                                       SIMILARITY: Belongs to the delta endotoxin family.
                                                                                                                                                                                                                                                                                                                                                                                                     1109
240
106
242
114
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Matches:
Conservative:
Mismatches:
Indels:
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HSSP; Q06117; 1JT6.
INTERPO; PRR001179; Endotoxin.
InterPo; IPR005638; endotoxin_C.
InterPro; IPR005639; endotoxin_N.
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SEQUENCE [GENOMIC DNA]
                                                                                                                                                                                                                                                                                                                                                                     1109 AA; 125714 MW;
                                                                                                                                                                                                                                                                                                                     Pfam; PF03944; Endotoxin C; 1.
Pfam; PF00555; Endotoxin M; 1.
Pfam; PF03945; Endotoxin N; 1.
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901.00
49.29%
34.19%
22.87%
                                                                                                                                                                                                                                                                                                                                                         Sporulation, Toxin.
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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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TyrAspGluLeuLeuValTyrileGluLysTyrileAsnTyrCysThrLysThrTyrHis
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PRINTIPLEUSETAED
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336 Asn-----ThrAsnArgLeuSerLysGlnLeuIleThrLeuLeuProGly
                                                                                                                                                                     TGGAATGCAGATATACATCCTTCACAAATTGAACCTAATGCTGGAACATCAGATGACTAT
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182 IleAsplysAspleuAspMetLeuLysAsnAsnAsnAlaSerTyrArgIleFroThr----- 199
SIMILARITY: Belongs to the delta endotoxin family.
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251
1114
268
128
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                       EMBL; M12662; AAA22614.1; -; Genomic_DNA.
PIR; B29838; B39838.
InterPro; IPR001178; Endotoxin.
InterPro; IPR005638; endotoxin_C.
InterPro; IPR005639; endotoxin_N.
                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR005639; enc...
Pfam; PF03944; Endotoxin C; 1.
Pron0555; Endotoxin M; 1.
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897.00
47.96%
32.98%
22.77%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Toxin.
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Query Match:
DB:
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Percent Similarity:
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SEQUENCE 6
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                                                                   AACAGICTIGATACAAACICTAAGGIAATIGAAGGACCIGGICATACAGGAAGGAAACITG 1767
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Walfield A.M., Pollock T.J.;
Walfield A.M., Pollock T.J.;
"Structural similarity between the lepidoptera- and diptera-specific
"Structural similarity between the lepidoptera- and diptera-specific
"Structural similarity between the lepidoptera- and diptera-specific
"Structural and 'Israelensis'.";
J. Bacteriol. 166:801-811(1986).
-!-FUNCTION: Promotes colloidosmotic lysis by binding to the midgut
epithelial cells of mosquitos. Active on Aedes aegypti.
-!- DEVELOPMENTAL STAGE: The crysteal protein is produced during
sporulation and is accumulated both as an inclusion and as part of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ValAsnSerGlnAsnLeuIleSerGluSerValSerThrGlnIleProLeuValLysAla
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                                                                                                               ::: ||||||:::||| | TyrGluVal---ThrAsnAsnSerVallleArgGlyProGlyPheThrGlyGlyAspLeu
                                                                                                                                                                                                    GTTTATTTACAAAGTCAAGGCCGTTTAGAGATTACATGTAGAACTCCTAATTCTACACAA
                                                                                                                                                                                                                                      1828 TCTTATTACATTAGACTTCGATACGCTACAAATGGTGCTGGAAATACTCTTCCTAATATA
                                                                                                                                                                                                                                                                                                                                                                                              LystyrAlaileSerLeuPheTyrAlaAlaAsnAsnAlaIleAlaValSerIleAspVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                              1888 TCTCTTACAATACCAGGAGTAATAGGAATACCACCTCAACGACTCAACAACACTTTTTCT
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01-MAR-1989 (Rel. 10, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
13-SEP-2005 (Rel. 48, Last annotation)
13-SEP-2005 (Rel. 
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MEDLINE=86223796; PubMed=3011746;
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C10AA BACTI
C10AA BACTI
D C10AAR.
DT 01-MAR.
DT 13-SEP.
DE CYCXA (a. GN)
NAMMESTI
DE BACILIUM
OC CO -1- DEVICO
CC -1-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATAATATCITITIGGTACCCTAATCACTGTCTTTTGGCCCGGGGGAGAACAAGACAAAACA 372
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| AsnLysAsnGluTyrGluIlePheAsnAlaProSerAsnGlyPheSerLysSerAsnAsn
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1915 ATACCACCTCAACGACTCAACACACTTTTTCTGGTACAAATTATAAT-----AATTTA 1968
                                                                                                               1855 ACAAATGGTGCTGGAAATACTCTTCCTAATATGTCTTTACAATACCAGGAGTAATAGGA 1914
                                                                                                                                                                                                                                       2011 -----ACATTACCTTTAAATCGAAACATACCATTTATATTTAATCGTGCAGATGTA 2061
                                                                                                                                                                                                                                                                                                                       GAAGGACCTGGTCATACAGGAGGAACTTGGTTTATTTACAAAGTCAAGGGCGTTTAGAG
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ThrAsnAla-------ProLysThrThrValPheLeuThrGlylleAspThr
                                                                                                                                                                                                           601 ThrTyrAlaAspPheGlyTyrValThrPheProArgThrValProAsnLysThrPheGlu
                                                                       1798 ATTACATGTAGA---ACTCCTAATTCTACACAATCTTATTACATTAGACTTCGATACGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Name=cry10AA; Symonyms=cry1VC, cryXA(A), pBt047;
Bacillus thuringlenais (subsp. israelensis).
Bacteria, Firmicutes; Bacillales; Bacillus;
Bacillus cereus group.
                                                                                                                                                                                               1969 CAATACGGAGATTTTGGGTATTTCCAATTTCCAAGTACAGTA
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Last annotation update)
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OBKNV2;
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360 AspProTyrAspIlePheSerPheThrGlyAsnGlnMetAla------373
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                                                                                                                                  274 ThrIrpasnMetTyrasnThrTyrargLeuGluMetThrLeuThrValLeuAspLeuIle 293
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                                                                                                                       AACTATTGTGCAAATACCTATAGAGAAGGACTAAATAAACTTCGAAACGAACCTAATATG
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                                       GGTGCTGAATTGGCTGATGGAATGCAGATATACATCCTTCACAAATTGAACCTAAT
                                                           217 AlaAlaThrTyrTyrAsnIleTrp-----LeuGlnAsnGlnGlyileAsnProSer
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SQ SEQUENCE	NCE 675 AA;	77759 MW;	4EB0E51AA0372FF1	L CRC64;		ï	
Alignment	Scores:					g G	
Pred. No.:		2.46-52	Length: Matches:			È	952 GCT(
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ò	715 GGTGCTGAA	ATTGGCTGATGA	ATGGAATGCAGATATAC	GGTGCTGAATTGGCTGATGAATGGAATGCAGATATACATCCTTCACAAATTGAACCTAAT	AT 774	ò	
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AGGACCTGGTCATACAGGAGGAAACTTGGTTTATATAAAGTCAAGGGCGTTTAGAG 1797 AAATGGTGCTGGAAATACTCTTCCTAATATATCTCTTACAATACCAGGAGTAATAGGA 1914 ACCACCTCAACAACAACAACATTTTTTCTGGTACAAATTATAAT-----AATTTA 1968 TAATCAAATTGAACTTTAATTTAAATAATTCACCTAGTAATAAATTAACATATTCAGCT 1437 3GGGAATTTATCTAATGATAAAAACAACTGATTTTCAATTTCCTGTAAAAAAGAC 1497 CCAGITITICITITATITIAAITIATICCIALAAATIGGAITAGCGCIAAAIATATATAT 1617 AGGTGCATTAGGATGGACACACAGTAGTGTTAATAGAAATAATGCAATATCAGATAAA 1677 IACATGIAGA---ACTCCIAATICIACACAATCTTATTACATTAGACTTCGATACGCT 1854 ATTATTTTCATTTTTAGATGAACTTATTTTTTATACAAAAAT--------1176 AACGTAC---------GGGAATCGTTTAGTTGGTATTGCGAATCGTAAT 1218 CCACCCACAACAAAAACTTTAATACCATTTGAATCCTAT------AAAGTT 1317 AATTGTAACTGATAGACAAGTAACTCCTACTTCCCCTTTTCCTAACATATACTTTACA 1377 FAAACCAATTATTAATCCAAATTGTTTACCAAGCTATAATAGTTATAGTCATATTTTA 1557 AATTACAATGATCCCAGCAATCAAAGGTAACAGTCTTGATACAAACTCTAAGGTAATT 1737 ICAATTITITITIATGATATAAAGAGATACAAAGATTCAATAGGAAGAATAGGTGGC 1011 CCTTGAAATTCAACCCAATCTCGCTATAATGGAATATAATTTAACACGTTCAGGGCTT 1131 ::: |||::: ||| |||||| |||||| serThrileGluAsnAsnTyrLysArgThrAspSerTyrMetIleGluAsnAsnTyrLysArgThrAspSerTyrMetIleProLysGlnThr 461 plys-----panlysGluTyrGlyHisThrLeu 471 | ||||||| ;;; ;;; rTyrlleLygThrAspAsnTyrllePheSerVal------ValArgGluArgArg 488 |||||| ||| |||| |||:::|||| nileThrGlnileHisAlaLeuLysAlaLeuLysValSerSerAspSerLysIleVal 528 SerGlnAspThrSerLysValPheProPheTyrArgAsnLysProIleAspLysVal 412 : |||| oproTyrAspIlePheSerPheThrGlyAsnGlnMetAla-------373 PheThrHisThrAsnAspAspArgAsnIleIleTrpGlyAlaValHisGlyAsnIle 392 ||||||| ulleValArgHi8ArgGlu------TyrSerAsp 422

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TATGATATAAAGAGATACAAAGATTCAATAGGAAGAATAGGTGGCATTAAAACTGAACTT 1026
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166 ProAsnSerThr-----AsnThrThrThrValArgGluArgPheGlnGluValAsn 182
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297 TyrAspProArgLeuTyrLysGluArgLeuSer------ValGluIleLeu 311
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ThrArgLysLeuTyrThrAspProIleAsnTyrHisArgGlyIleSerLeuGluAlaAsp 331
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ThrAsn-----ThrTyrArgTyrLeuSerProAspLysIlePheAlaGluArg 377
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                             GAGACATTTGCTAGTGCTGATACAATTGCTGCAGTTAGTGCAGGTACTATTGTATTCCGGT
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                                                        GluAlaAsnLeuGlnAsnSerLeuValGlyLeuPheAlaIleThrAlaAlaIleAlaSer
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                                             GlyGluAspThrLeuLeuMetThr------LeuTyrGlyThrProAsnHis
                                                                                                                                          TCAAATTCAATTTAAATCATTGATAAAATTGAATTTATACCAATTACTTCCTCTGTACGC
                                                                                                                                                          2011 -----ACATTACCTTTAAATCGAAACATACCATTTATATTTAATCGTGCAGATGTA
                                                                                                                                                                                                                                                                                                                        D OBVIXZ BACTV PRELIMINARY; PRT; 650 AA.
C 08VIXZ.
T 01-WAR-2002 (TrEMBLrel. 20, Created)
T 01-WAR-2004 (TrEMBLrel. 20, Last sequence update)
T 01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
E Cry29Aa protein.
N Name=cry29Aa;
N Name=cry29Aa;
S Bacillus fuhuringiensis (subsp. medellin).
C Bacteria; Firmicutes; Bacillales; Bacillus (subsp. medellin).
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Delectue A., Orduz S.;
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AJS1977; CAG0998:1, -; Genomic DNA.

GO; GO:0016707; F:hydrolase activity; IEA.

GO; GO:0005902; F:receptor binding; IEA.

GO; GO:0006952; P:defense response; IEA.

GO; GO:0009405; P:pathogenesis; IEA.

InterPro; IPR00179; Endotoxin.

InterPro; IPR005639; endotoxin.
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                            CAATACGGAGATTTTGGGTATTTCCAATTTCCAAGTACAGTA-
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Matches:
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Pfam; PP00555; Endotoxin M; 1.
Pfam; PP03945; Endotoxin N; 1.
SEQUENCE 650 AA; 74435 MM;
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32.38$
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Best Local Similarity:
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Asn 675
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1267 ACAGGTCCACCACAAAAAACTTTAATACCATTTGAATCCTAT-----AAAGTTTCA 1320
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|IleThrGlnIleProAlaValLy8AlaTyrGlnLeuGlyValGlnSerGlnValIleLy8 501
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SerCysGlnHisLeuSerAsnValThrLysLysTyrPheValArgIleArgTyrAlaThr
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P05519; P11782; P16479;
01-NOV-1988 (Rel. 09, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
13-GSP-2005 (Rel. 48, Last annotation update)
Pesticidial crystal protein cry4Ba (Insecticidal delta-endotoxin
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its
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                                                                                                                   MUCLEOTIDE SEQUENCE.
MUCLINE-88157738; PubMed=2831510;
MEDLINE-88157738; PubMed=2831510;
MEDLINE-88157738; PubMed=2831510;
MIDIPREDUBLY S., Settemation C., Panyim S.;
"The complete nucleotide sequence of a 130 kDm mosquito-larvicidal delta-endotoxin gene of Bacillus thuringiensis var. israelensis.";
Nucleic Acids Res. 16:1637-1638(1988).
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Floning and nucleotide sequences of the two 130 kDa insecticidal
protein genes of Bacillus thuringiensis var. israelensis.";
Agric. Biol. Chem. 52:873-878(1988).
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crystal
                                                            Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
Bacillus cereus group.
WCBI_TaxID=1430;
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CryIVB(a)) (Crystaline entomocidal protoxin) (128 kDa
                         yD2, cryIVB(a), isrH3;
israelensis.
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EMBL; X05692; CAA29174.1; -; Genomic_DNA.

EMBL; D00247; BAA00178.1; -; Genomic_DNA.

EMBL; X07423; CAA30317.1; -; Genomic_DNA.

EMBL; X07423; CAA30312.1; -; Genomic_DNA.

PIR; S00399; USBS81.
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NUCLEOTIDE SEQUENCE.
STRALN-4Q2-72;
MEDLINE-88185334; PubMed-2833395;
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InterPro; IPR001178; Endotoxin.
InterPro; IPR005638; endotoxin_C.
InterPro; IPR005639; endotoxin_V.
Pfam; PF03944; Endotoxin_C; 1.
                               cryD2,
                                                                                                                                                                                                                                                                                                                                                  Eur. J. Biochem. 173:9-16(1988)
                            Name=cry4Ba; Synonyms=bt8, cry
Bacillus thuringiensis subsp.
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NUCLEOTIDE SEQUENCE.
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Pfam; PF00555; Endotoxin_M; 1.
Pfam; PF00555; Endotoxin_M; 1.
Pfam; PF00345; Endotoxin_M; 1.
Patructure; Plaemid; Sportlation; Toxin.
NFLICT 193 201 K. P. D (in Ref. 4).
VELICT 193 201 K. PKCTRWY (in Ref. 4).
VELICT 203 204 R. S -> C (in Ref. 3).
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SerTyrArgThrAlaVallleThr-----GInPhe---AsnLeuThrSerAlaLys 156
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ThrProThrProGluGlyLeuArgThrThrPhePheGlyPheSerThrAsnGluAsn--------TATAAAGTTTCAATTGTAACTGATAGACAAGTAACTCCTACTTCCCCTTTTCCT :::||| |||:::::: 393 ValThrLysMetAspPheTyrLysIleAspGlyThrLeuAlaSerTyrAsnSerAsnIle 1501 AAACCAATTATTAATCCAAATTGTTTACCAAGCTATAATAGTTATAGTCATATTTTATCC TTAGATGAACTTATATTTTATACAAAAATGAAACGTACGGGAAT-------1423 TTAACA-----TATTCAGCTGGGGGGAATTTATCTAAT-----157 670 730 197 850 910 970 268 288 1147 321 1309 1456 413 1561 358 388 ద ò 셤 셤 ઠ ઠ 셤 8 셤 ઠ 8 8 셤 8 셤 ઠે g 8 8 8 & 8 ठ 8 8 8 8 8 요 요 용 à 셤 ð

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MEDLINE=22235415; PubMed=12324359;
DOI=10.1128/AEM.68.10.5082-2505.2002;
DOI=10.1128/AEM.68.10.5082-2505.2002;
Berry C., O'Niel S., Ben-Dov B., Jones A.F., Murphy L., Quail M.A., Harris D., Zaritsky A., Parkhill J.;
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Appl. Environ. Microbiol. 65.5082-5095(2002).
EMBL, A.731825, CAD30095.1; -; Genomic DNA.
SEQUENCE 1136 AA; 127763 MW; BAC4E8C26FE3E9B5 CRC64;
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10-MAZ-2005 (TYEMBLrel. 30, Last sequence update)
10-MAY-2005 (TYEMBLrel. 30, Last annotation update)
10-MAY-2005 (TYEMBLrel. 30, Last annotation update)
Pesticidial crystal protein cry4BA.
Name-cry4BA; Synonyms-BTB, cryD2, cryIVB(A), isrH3, pBt038;
Bacillus thuringienais (subsp. israelensis).
Bacteria; Firmicutes; Bacillales; Bacillus cereus group.
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157 LeuArgGluThrAlaValTyrPheSerAsnLeuValGlyTyrGluLeuLeuLeuLeueuPro
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                                                                                                                                                                                                                                                                                                                                    AGTGCTGATACAATTGCTGCAGTTAGTGCAGGTACTATTGTATCCGGTACTCTGTTAGCC
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-----SerAlaValLeuProIleLeuTrpProThrAsnThrProThrProGluArgVal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             670 ATTTATGCGCAAGCTGCTAATTTTCATTTAAATTTATTACAACAAGGTGCTGAATTGGCT
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1136
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268
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                  Matches:
Conservative:
Mismatches:
Indels:
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4.97e-47
819.00
47.70%
32.33%
20.79%
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7.18e-46
801.50
46.82%
32.36%
20.35%
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01-MAR-2002 (TrEMBLrel. 20,
01-MAR-2004 (TrEMBLrel. 26,
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QBVNX1;
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Best Local Similarity:
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TTAGATGAACTTATATTTTATACAAAAATGAAACGTACGGGAAT------ 1191
                                                                                                                                                                                                                                                                                                                                                                                  -----CAGTTTTCTTTATTTATTAT---TCCTATAAAATTGGATTAGCGCTAAATATA 1611
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393 ValThrLysMetAspPheTyrLysIleAspGlyThrLeuAlaSerTyrAsnSerAsnIle 412
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                                     CCCAATCTCGCTATAATGGAATATAATTTAACACGTTCAGGGCTTAGATTATTTCATTT
                                                                                                                                                                      ---IleTyrGlySerSerGlyPheGlySerAsnLeuThrHisGlnIleGlnLeuAsnSer
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Name-cry30Aa;
Name-cry30Aa;
Bacillus thuringiensis (subsp. medellin).
Bacitlus thuringiens; Bacillales; Bacillus;
Bacillus cereus group.
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NUCLECTIDE SEQUENCE.

NUCLECTIDE SEQUENCE.

Submitted (DEC-1999) to the EMBL/GenBank/DDBJ dat EMBL, AJ51978; CAC80986.1; -; Genomic DNA.

GO; GO:0016797; P:hydrolase activity; IEA.

GO; GO:000592; P:receptor binding; IEA.

GO; GO:0005952; P:defense response; IEA.

GO; GO:0009405; P:pathogenesis; IEA.

GO; GO:0009405; P:pathogenesis; IEA.

GO; GO:0009405; P:pathogenesis; IEA.

R InterPro; IPR001178; Endotoxin.

R InterPro; IPR005539; endotoxin.

R Pfam; PF03944; Endotoxin.

R Pfam; PF03944; Endotoxin.

R Pfam; PF0355; Endoto
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ACAATTAATCAAATTGAACTT 1395 ||||||||::::: ---IleAsnGluMetSerPhe 434 AAAATAATTACAATGATCCCA 1695 |||||| ABNAXGIleThxGlnIlePro 530 ATTGAAGGACCTGGTCATACA 1755 CAAGGGGTTTAGAGATTACA 1803 ||| :::::||| SerGlyThrMetGlnIleGln 570 ACAATACCAGGAGTAATAGGA 1914 |||:::|||| |hrLeuLeuGlyGlnThrArg 608 -----ACAGTAACATTACCT 2019 |||:::|||||||| |lelleThrMetThrLeuPro 648 GATGTATCAATTCAATTTTA 2076
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GlyLeuLeuAsnAsnGlnLeu 668 STITCAATIGIAACTGAIAGA 1335 AAT-----TTATCTAAT 1455 31nAsnAlaLeuileSerAsn 474 SACTGTAAACCAATTATTAAT 1515 TATCCCAGTTTTCTTTATTT 1575 ATACAGGTGCATTAGGATGG 1635 TACATTAGACTTCGATACGCT 1854 :::||||:::|||||||||| GlyLeuArgMetArgTyrAla 590 AATTAT-----1965 .---- 1407 ::: ::: PheGlyTyrSerPheAlaTrp 510 ::: AsnAsnIleIleProThrAsp 628 ||| || ||| ||| slyProValArgGluGlyThr 398 /alHisTyrSerAlaGlyGlu 454 475 |||||| LeuSerAspIleLysMet--- 490 GTA 2118 |||| Val 682

888

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949 ATCGCTCAATTTTCTTTTTATGATATAAGAGATACAAAGATTCAATAGGAAGAATAGGT 1008
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     ATGAGATGGAGTATATTTAATGATTATCGAAGATATATGACTATTACTGTATTAGATACT 948
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|SerSerIleAlaGly------IleSerAspMetThrPheTyrLysSerAspTyr 439
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|GlnArgGlyAlaValTyrGlyAspAspTrpGluLysAspIleAsnGlySer---IleSer
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AlaThrLysThrGluLeuThrArgLysIleTyrMetProSerPheGlyLeuGlnGer
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                                                         TTTGAGAATGTTCACAATGATTTTATTCGAGAAATACCTGGTTTCCAACTTGAA---ACT
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PheAspSerValArgAspLysVallleAspLeuLysAsnAspTyrMetIleAsnProGlu
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                                                                                                                               649 TATAAAACGCTATTACTACCTATTTATGCGCAAGCTGCTAATTTTTCATTTAAATTTATTA
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129 GlnAspAlaIleGluIleLeuValThrGlyValLysSerGlyTyrAsnAlaLeuLysAsn 148
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|GuTyrGluIleLeuAspAla----LeuProAsnTyrSerAsnMetValAsnAlaTyr 26
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                                                                                                                                                                                H., ABano S.;
databases.
                                                                         Bacillus;
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   annotation update)
                                                                                                                                                                         Ikeyar T., Yamaya K., Ito T., Sahara K., Bando H., Submitted (OCT-2003) to the EMBL/GenBank/DDBJ datic BMBL, AB125059; BAD00052.1; -; Genomic DNN. GO; GO:001679; P: Phydrolaee activity; IEA. GO; GO:000592; P: Pieferber response; IEA. GO; GO:000592; P: Pieferber response; IEA. GO; GO:0009405; P: Pieferber response; IEA. GO; GO:0009405; P: Pieferber REA. GO; GO:0009405; P: Pieferber REA. InterPro; IPR005639; endotoxin. C. InterPro; IPR005639; endotoxin. C. InterPro; IPR005639; endotoxin. N. Pfam; PF03944; Endotoxin. M. Pfam; PF03945; Endotoxin. M. Pfam; PF03955; Endotoxin. M. SEQUENCE 683 AA; 77438 MW; 4888477B876BFDCA C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length:
Matches:
Conservative:
Mismatches:
                                      Bacillus thuringiensis (subsp. entomocidus).
Bacteria, Furmicutes; Bacillales; Bacillaceae;
Bacillus cereus group.
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05-JUL-2004 (TrEMBLrel. 27, L.
Putative mosquitocidal toxin.
Name=cry30Aa like;
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796.00
45.13%
31.41%
20.21%
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Best Local Similarity:
Query Match:
DB:
                                                                                                                                                            STRAIN=INA288;
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Pfam; PF03945; Endotoxin_N; 1.
Spornlation; Toxin.
SEQUENCE 1169 AA; 133544 MW
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Query Match:
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IleLeuSerAspIleLysMetIleTyrPheArgThrGlyGlyMetTyrGlnValTyrAsp 502
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-!- FUNCTION: Promotes colloidosmotic lysis by binding to the midgut
epithelial cells of insects. Active on various scarabaeid beetles.
-!- DEVELOPMENTAL STAGE: The crystal protein is produced during
sporulation and is accumulated both as an inclusion and as part of
the spore cost.
                                                                        |||||||:::|||
ProAlaValLysAlaLeuGlyIleSerThrAspSerLysValValLysGlyProValPhe
                                                                                                                                                           -----TTAATCATTGATAAAATTGAATTTATACCAATTACTTCCTCTGTACGCCAA
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                                                             TGGACACACACTAGTAGTAATAGAAATAATGCAATATCAGATAAAATAATTACAATGATC
                                                                                                      CCAGCAATCAAAGGTAACAGTCTTGATACAAACTCTAAGGTAATTGAAGGACCTGGTCAT
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---GluPhelleMetAspLysProSerIleAspValAlaIleArgGlyValGlnAsnAsp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE [GENOMIC DNA].
STAALN=MRKL B-18746 / PSSOC;
Michaels T.B., Poncersada L., Narva K.B.;
Process for controlling scarab pests with Bacillus thuringiensis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
11-SEP-2005 (Rel. 48, Last annotation update)
Pesticidial crystal protein cry8Ba (Insecticidal delta-endotoxin CryVIIIB(a)) (Crystaline entomocidal protoxin) (134 kDa crystal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein).
Name-cry8Ba; Synonyms=50C(b), cryVIIIB(a);
Bacillus thuringlensis subsp. kumamocoensis.
Bacteria; Pirmicutes; Bacillales; Bacillaceae; Bacillus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT; 1169 AA
                                       PheGlyTyrserPhe----
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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MISCELLANEOUS: Toxic segment of the protein is located in the
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216
152
297
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                       terminus.
SIMILARITY: Belongs to the delta endotoxin family.
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Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (1-1169)
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HSSP; P07130; 1DLC.
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InterPro; IPR005638; endotoxin.
InterPro; IPR005639; endotoxin.N.
Pfam; PF03944; Endotoxin.C; 1.
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1654 AGAAATAATGCAATATCAGATAAATAATTACAATGATCCCAGCAATCAAAGGTAACAGT 1713
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QSW7N9;
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Bacteria, Firmicutes; B:
Bacillus cereus group.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1288 ACTITA----TCAATTGTAATCCTATAAAGTT---TCAATTGTAACT 1329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTTTCTTTTTATGATATAAGAGATACAAAGATTCAATAGGAAGAATAGGTGGCATTAAA 1017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAAAATGAAACGTAC---GGGAATCGTTTAGTTGGTATTGCGAATCGTAATAGATCTACT 1227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AATAAATTAACATATTCA---GCTGGGGGAATTTATCTAATGATAAAAAAACAACTGAT 1473
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                                                                                                                                                                                                                                                                                                                                                                                 266 IleAbpTyrAsnGlnPheArgArgGluMetThrLeuThrValLeuAspValValAlaLeu 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |||||| |||||| ::: ||||
286 PheSerAsnTyrAspThrArgThrTyrProLeuAla-------ThrThr 299
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315 AspVal---ProAsnileGlySerTrpTyrAspLysAlaProSerPheSerGluIleGlu 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              :::||| :::||| 432 ProGluThrGluPhePheMetValAsnGlnLeu------AsnAsnThrArg 446
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  300 AlaGinLeuThrArgGluValTyrThr-------AspProLeuGlyAlaVal 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ||| ::: |||| ||| ||| ||| TyrLysHislleGlyThrSerSerThrPheThrGlnWetTyrGly-----ThrAshGln 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      392 AsnLeuGlnSerThrSerAsnPheAspPheThrAsnTyrAspIleTyrLysThrLeuSer 411
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                                     CTATTACTACCTATTTATGCGCAAGCTGCTAATTTTCATTTAAATTTTACAACAAGGT 717
                                                                             ProPheLeuThrValTyrThrMetAlaAlaAsnLeuHisLeuLeuLeuLeuArgAspAla 214
                                                                                                                                                                                                  GGAACATCAGATGACTATATAAAACTTTTAAAAGAAAATATACCTAAATATAGTAACTAT 837
                                                                                                                                                                                                                                                                             TGTGCAAATACCTATAGAGAAGGACTAAATAAACTTCGAAACGAACCTAATATGAGATGG 897
IleLeuAspSerLeuPheThrGlnTyrMetProSerPheArgValThrAsnPheGluVal 194
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SerSerThrSerThrTyrValProValPheSerTrpThrHisArgSerAlaAsp
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LeuThrAspArgIleGlySerCysGluPheGlnMetIlePheProGluSer---GlnArg
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Identification and characterization of novel cry genes from an "Identification and characterization of novel cry genes from an megquito-specific Bacillus thuringiansis serovar sotto strain.";

L. Submitted (OCT-2004) to the EMBL/GenBank/DDBJ databases.

R. Submitted (OCT-2004) to the EMBL/GenBank/DDBJ databases.

R. OG OCO:001678; F. Phydrolase activity; IRA.

R. OG OC:0005102; F. Preceptor binding; IRA.

R. OG: OC:000592; P. Pietense response; IRA.

R. OG: OC:00049405; P. Piethogeneals; IRA.

R. OG: OC:0030435; P. Piethogeneals; IRA.

R. InterPro; IRRO05139; Endotoxin.

R. InterPro; IRRO05538; endotoxin.

R. Pfam; PF03944; Endotoxin.

R. Pfam; PF03945; Endotoxin.

R. Pfam; PF03945; Endotoxin. N; 1.

R. Pfam; PF03945; Endotoxin. N; 1.

R. Pfam; PF03945; Endotoxin. N; 1.
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LysAspGlyLeuGlnProGlyValThrAspTyrGluValAsn 695
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Last annotation update)
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Alignment Pred. No.: Score: Percent Si Best Local Query Matc	Alignment Scores: Pred. No.: Score: Percent Similarity: Best Local Similarity: Query Match:	9.456.43 755.50 46.428 31.968 29.188	Length: Matches: Conservative: Mismatches: Indels:	688 241 109 129 33	
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∂ 8	13 AATAATAAT 6 AenLyeaer	AATAATAATGAATATGAGATTATC ::: AsnLysAsnAspSerGluIleLeu	TCGATTCAAAGAATTTAT ::::::: euAsnAlaSer5	AATAATAATGAATATGAGATTATCGATTCAAAGAATTTATCTTATCCTTCTAACAGAAAT	72
È	73 ATTGATCAT	rrctagataccttac	PACAAATAATCCAAATC		132
ପ୍ଧ	24 ThrThrTy	: :: rProLysTyrProLeu	::::: AlaHisSerArgGlnA	::: ::: ThrThrTyrProLysTyrProLeuAlaHisSerArgGlnAspSerMetGluAsnMetAsn	43
8 1		TACAAAGAGTGGCTCAATATGTGT	CAAGGGAATACACAA	TGATAATTTCGAGACA	192
8		uTrpileAsnGinCy6			9.0
රු සි	193 TTTGCTAG1 ::: 57 PheCysTh	TTTGCTAGTGCTGATACA ::: PheCysThrProlleAspThrAsp	ATTGCTGCAGTTAGTC ::: ::: oileAsnSerValAla7	TTTGCTAGTGCTGATAGAATTGCTGCAGTTAGTGCAGGTACTATTGTATCGGGT 	246 76
è	247 ACTCTGTTP	AGCCGGTATAGGTGGC	crcactrcrararcc	ACTCTGTTAGCCGGTATAGGTGGGCTCACTTCTATATCCGGACCGATAGGAATAATAGG	306
qq	77 AlaileLeuAl	 JAla	 LeuileProd	 -LeuileProGlyProGlyGluAlaileGly	06
È	307 GCTATAATA	AATATCTTTTGGTACC	CTAATCACTGTCTTT	GCTATAATAATATTGGTACCCTAATCACTGTCTTTTGGCCCGGGGGAGAACAAGAC	366
qq	91 PhevalLeu	.serThrPheThrSer	PhevalLeuSerThrPheThrSerLeulleProTyrLeuTrpProSer	AspThr	108
ò	367 AAAACAGTA	AAAACAGTATGGACACAATTTTATTAAAATGGGA		-GAAATTTTTGTTGATACACCGTTA	423
g G	109 LysLysile	errpGlyAspPheThr	LysglnglyLeugln	PheArgProGluLeuGly	128
È	424 ACAGAAAGCATAAAA-	CATAAAA	CAGCTAL		465
ପୁ	129 AsnAspAla	aileGlullelleGly	/AsnAspValĠinSer(AsnAspAlaileGluIleIleGlyAsnAspValGinSerGluTyrAsnSerLeuLysThr	148
č		AATATTACAAAGCTAT	PATACAGCATTAGATC		525
qa	149 Phe	MetĠińAsnPhe	GluAspSerPheThri		165
ò	526 CTACAAGCT	TCCTGGATTACCACC	ATCATCAGCATTACAAC		585
qq	166		Arg		173
장 옵	586 ATACGATT	TGAGAATGTTCACAAT ::: eSerSerValArgAsp	rgartrarrcgagaa 	ATACGATTTGAGAATGTTCACAATGATTTTATTCGAGAAATACCTGGTTTCCAACTTGAA	645 193
à	646ACTTA	TAAAACGCTATTACT	ACCIATITATGCGCAA	-ACTITATAAAACGCTATTTACTACCTATTTAAGCTGCTAATTTTCATTTAAAT	702
QQ	194 ProGluAsı	 nLysProAlaPheLe	.:: 	ProGluAsnLysProAlaPheLeuIleLeuTyrAlaGlnThrAlaAsnPheAspLeuIle	213
ò	703 TTATTACA	ACAAGGTGCTGAATTC	SCCTGATGAATGGAAT	TTATTACAACAAGGTGCTGAATTGGCTGATGGAATGCAGATATACATCTTCACAA	762
qq	214 LeuTyrdi	nArgGlyAlaLeuTy:	rAlaAspGluTrpGlu	euTyrGlnArgGlyAlaLeuTyrAlaAspGluTrpGluAsnAspIleAsnArgSer	232
È	763 ATTGAACC	TAATGCTGGAACATC	AGATGACTATTATAAA(AITGAACCIAATGCTGGAACATCAGATGACTATTATAAACTTTTAAAAGAAATATACCT	822
gg Gg	233 ileSerPr	orenteudlyser	rLysAsptyrtyrile	leserProLeuLeudlySerLysAspTyrTyrlleSerLeuAlaAlaLyslleLys	251
<i>ት</i> 8	823 AAATATAG ::: :: 252 GluTyrTh	TAACTATTGTGCAAA	IACCTATAGAGAAGGA uThrTyrArgAsnSer	AAATATAGTAACTTTGTGCAAATACCTATAGAGAAGGACTAAATAAA	882
È		GAGATGGAGTATATT:	TAATGATTATCGAAGA	CCTAATATGAGATGGAGATATTAATGATTATCGAAGATATATGACTATTACTGTATTA	942

aLeu 291	AAGA 1002	TGAC 1062 uGln 325	ACGT 1122 rHi8 342	AACG 1182 uAsn 361	1206 rThr 381	AAGA 1266 -Arg 395	rgra 1326 : u 414	AATT 1380 : rile 426	raat 1419 : rthr 446	TCAA 1479 tA8n 464	TAAT 1539 eLys 478	ATTA 1599 yThr 497	AAAT 1659 ::: oAsp 517	TGAT 1719 uThr 537	A 1776 		1866 18er 597	AGGA 1905 GThr 617
hrLeuGlyAl	ATTCAATAGG legln	AAATAAATTT erPheGlyLe	ATAATTTAAC snalateuTh	CAAAAAATGA hrilearggi	leSerArgTy	TATATGGAGA	AAGTTTCAAT ::: :: ysLeuSerLe	TATACTTTAC ::::: sluCysTyrSe	ATTCACCTAG ::: :: \BnAlaProTh	\CAACTGATTI \snThrPheMe	TACCAAGCTA	ataaaattgg agthrglygl	GTGTTAATAG servalasnPr	SGIAACAGICI ::: \laAspIyrLe	rrggrrrarrr euvalalare	CTAATTCTAC ::: 	CT	TTACAATACC
eSerTrpGlyThrTyrAsnLysTyrArgArgGluValThrLeuGlyAlaLe	GATACTATCGCTCAATTTTTGTTTTTATGATATAAAGAGATACAAAGATTCAATAGGAAGA 	ATAGGTGGCATTAAAACTGAACTTACAAGAGAAATTTATACAACTGAAATAAAT	CGTCTTACTTACCTTGAAATTCAACCCAATCTCGCTATAATGGAATATAATTTAACACGT :::	TATATTTATA 	TACGGGAATCGTTTAGTTGGTATT	AACTGAAATTA yval	acaggiccaccacaacaaaaactitaataccatitgaatcctataaagtitcaatigta AsnGlythrprothrGlnIleGlyLeuasnasnLeupheValtyrLysLeuSerLeu	ACTGATAGACAAGTAACTCCTACTTCTTCCTAACATATACTTTACAATT	AATCAAATTGAACTTTATTTAAATAATTGCCTAGTAAT 	aaattaacatattcagctgggggatttatctaatgataaaaaacaactgattttcaa ::: glnThrTyrGlnalaGlyargasnSerasnasnPhelleasnThrPheMetasn	TTTCCTGTAAAAAAAGACTGTAAACCAATTATTAATCCAAATTGTTTACCAAGCTATAAT	AGTTATAGTCCATTTTTATCCCAGTTTTCTTTTTAATTATTCTATAAATTGGATTA :::	GCGCTAAATATATATATACAGGTGCATTAGGATGGACACACAGTAGTGTTAATAGAAAT ::: ::: TyrprosertyrasppheGlyfyrserpheAlatrpthrhisthrServalasnbroasp	AATGCAATATCAGATAAATAACAATGATCCAGGAATCAAAGGTAACAGTCTTGAT 	ACAAACTCTAAGGTAATTGAAGGACCTGGTCATACAGGAAGGA	CAAAGTCAAGGGGTTTAGAGATTACATGTAGAACTCCTAATTCTACA 	-caatcttattacattagacttcgataggctacaaatggtgct	GGAAATACTCTTCCTAATATATTCTTTACAATACCAGGA
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ThrAsnIleSerTry	CTATCGCTCA euAlaAlaLe	GTGGCATTAA: ThrLy	TTACTTACCT serAenTyrPho	GGCTTAGATT	3GG	ATCGTAATAG	SGTCCACCCAC 31yThrProTh	aatagacaagt	CAAATT SlyileSerae	rtaacatattc ThrTyrG1	CCTGTAAAAA 	FATAGTCATAT -:: ThrasnHisII	CTAAATATATT ::: ProSerTyrAs	GCAATATCAGA LeuileValPr	AACTCTAAGGT 	CAAAG AlaAlaThrGl	CAATCTTA ::: SerArgArgTy	SerTyrThrVa
272 ThrA	943 GATA 292 ABPL	003 ATAG	.063 CGTC ::: 326 GlnS	123 TCAG 343 ProF	183 TACG ::: 362 PheA	207 GCGP 382 GlnP	267 ACAG 396 AsnC	327 ACTO	1381 AATC 427 AlaC	1420 AAA7 ::: 447 Gln-	480 TTTC	540 AGT	1600 GCGC	1660 AATK 518 Asnl	1720 ACA ::: 538 Serl	777 558 AsnAle	1825 578 Ala	1867 598 Leu
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GTAATAGGAATACCACCTCAACGACTCAACAACACTTTTTCTGGTACAAATTATAATT 1965
                                                                                                                                                                                                     649 GlnAsnThrIleValThrIleAlaIleGlnGlnLeuAsnAlaPheProAsnAspGlnLeu 668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE [GENOMIC DNA].

WUCLINE-99369730; PubMed-9704107;

Hwang S.H., Saitoh H., Mizuki E., Higuchi K., Obba M.;

Hwang S.H., Saitoh H., Mizuki E., Higuchi K., Obba M.;

Ha novel class of mosgutiocidal delta-endotoxin, Cry19B, encoded by a Bacillus thuringiensis servora higo gene.";

Syst. Appl. Microbiol. 21:179-184(1998).

-! FUNCTION: Promotes colloidosmotic lysis by binding to the midgut epithelial cells of mosquitos.

-! DEVELOPMENTAL STAGE: The crystal protein is produced during sportlation and is accumulated both as an inclusion and as part of
                                                                                                       618 PheLeu------Thrasp
                                                                                 ACAGTAACATTACCT
                                                                                                                                                                 TTAAATCGAAACATACCATTTATATTTAATCGTGCAGATGTA---TCAAATTCAATTTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the spore coat. MISCELLANEOUS: Toxic segment of the protein is located in the N-
                                                                                                                                                                                                                                                                                                                                                                                                             16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Pesticidial crystal protein cry19Ba (Insecticidal delta-endotoxin CryXIXB(a)) (Crystaline entomocidal protoxin) (78 kDa crystal
                                                                                                                                                                                                                                                     ATCATTGATAAAATTGAATTTATACCAATTACTTCCTCTGTA 2118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus,
                                                                                                                                                                                                                                                                        SIMILARITY: Belongs to the delta endotoxin family.
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Conservative:
Mismatches:
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Name=cry19Ba; Synonyms=cryXIXB(a);
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InterPro; IPR001179; Bndotoxin.
InterPro; IPR005639; endotoxin.C.
InterPro; IPR005639; endotoxin.N.
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Pfam; PP0355; Endecoxin M; 1.
Pfam; PP03965; Endecoxin M; 1.
Plasmid; Sporulation; Toxin.
SEQUENCE 682 AA; 78491 MW;
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                                          CTTGAAATTCAACCCAATCTCGCTATA-----ATGGAATATAAATTTAACACGTTCAGGG 1128
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LysAlaGluLeuThrArgGluIleTyrSerAspValIleAsn---AspHisValTyrGly 312
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---HisAlaPheThrTrpLeuLysGlyPheArgPheValThrAsnSer1leAsnSerTrp
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LeuMetVal---ProTyrIleSerPheGluHisAlaGluSerLeuTyrThrArgArgPro
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"Bacillus Cry9 Family Members.";
Submitted (MAR-2005) to the EMBL/GenBank/DDBJ databases.
EMBL; AY971349; AAX78439.1; -; Genomic DNA.
ERQENCE 1169 AA: 132126 WW; 85DCOGD5083E3F43 CRC64;
                                                                                                                                                                                                                                                                                                                                   Bacillus thuringiensis.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
Bacillus cereus group.
NCBI TaxID=1428;
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Name=cry9Dbl;
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earch completed: January 12, 2006, 06:34:38 ob time : 290.5 secs

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delta-endotoxin; delta-endotoxin associate polypeptide;
expression cassette; transformation; transgenic; plant; bacteria;
lepidoptera; coleoptera; pest; pesticide; resistance;
pesticidal activity.
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Copyright (c) 1993 - 2006 Compugen Ltd.
                                                               - protein search, using frame_plus_n2p model
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                                                                                                                                                                                           isolated delta-endotoxin and delta-endotoxin-associated nucleic acids polypeptides, useful for killing lepidopteran or coleopteran pests or producing organisms with pesticide resistance.
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                                                                                                                          Koziel MG,
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       19-PEB-2004; 2004US-007B2020.
19-PEB-2004; 2004US-007B2196.
19-PEB-2004; 2004US-007B2141.
19-PEB-2004; 2004US-007B3570.
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N-PSDB; ADR89396.
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       CAGTITICTITATITAATTATICCTATAAAATIGGATTAGGGGCTAAATATTATATACA
                                ATTACAATGATCCCAGCAATCAAAGGTAACAGTCTTGATACAAACTCTAAGGTAATTGAA
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Koziel MG,

Carozzi N, Hargiss T, (ATHE-) ATHENIX CORP

2004-635574/61.

N-PSDB; ADR89398

20-FEB-2003; 2003US-0448632P. 20-FEB-2003; 2003US-0448633P. 20-FEB-2003; 2003US-0448810P. 20-FEB-2003; 2003US-0448810P. 20-FEB-2003; 2003US-0448810P. 19-FEB-2004; 2004US-00782020. 19-FEB-2004; 2004US-00782020. 19-FEB-2004; 2004US-00782141. 19-FEB-2004; 2004US-00782141. 19-FEB-2004; 2004US-00782141.

2004WO-US005829

20-FBB-2004;

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This sequence represents an isolated delta-endotoxin. Some of the delta-endotoxin coding sequences of the invention have alternative start codons, producing more than one protein from a single open reading frame. The nucleic acid sequences of the invention are useful in DNA constructs or expression cassettes for transformation and expression in plants and bacteria. The nucleic acids and corresponding polypeptides are useful for killing lepidopteran or coleopteran pests. Compositions containing the delta-endotoxins of the invention, and methods for their production, are useful for the production of organisms with pesticide resistance, specifically bacteria and plants. These organisms are useful for generating altered or improved delta-endotoxin or delta-endotoxin-associated proteins that have pesticidal activity, or for detecting the presence of delta-endotoxin or delta-endotoxin-associated proteins or nucleic acids in products or organisms.
                                                                                                                                                                                                                                                                                                                                 isolated delta-endotoxin and delta-endotoxin-associated nucleic acids polypeptides, useful for killing lepidopteran or coleopteran pests or producing organisms with pesticide resistance.
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delta-endotoxin, delta-endotoxin associate polypeptide; expression cassette; transformation, transgenic; plant; bacteria; lepidoptera; coleoptera; pest; pesticide; resistance; pesticidal activity.

Bacillus thuringiensis

WO2004074462-A2

02-SEP-2004

AXMI-007 alternative protein

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                                                                                                 GCTGAATTGGCTGATGAATGCAGATATACATCCTTCACAAATTGAACCTAATGCT
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                       TTACAAAGCTATAATACAGCATTAGATGATTGGAGAAAATTAAAAAGACTACAGCTCCT
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The presence of delta-endotoxin or delta-e
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20-FEB-2003; 2003US-0448632P.
20-FEB-2003; 2003US-0448833P.
20-FEB-2003; 2003US-0448863P.
20-FEB-2003; 2003US-0448810P.
20-FEB-2003; 2003US-0448810P.
19-FEB-2004; 2004US-00782020.
19-FEB-2004; 2004US-00782020.
19-FEB-2004; 2004US-00782040.
19-FEB-2004; 2004US-00782141.
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The 130 kDa delta-endotoxin from B. thuringiensis subsp. israelensisis is encoded by a 4.46 kb insert of pCH130. The protein is insecticidal and can be used to control insect pests esp. mosquitos. See also AAP94035. (Updated on 25-MAR-2003 to correct PA field.) (Updated on 27-MAG-2003 to
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112 AgnThr---TrpSerAgpPhelleThrGlnThrLygAgnIleIleLygLygGluIleAla 130
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TyrHisAsnHisLeuLysThrTrpGlu------AsnAsnProAsnProGln 165
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AsnLysAsnGluTyrGluThrLeuAsnAlaSerGlnLysLysLeuAsnIleSerAsnAsn
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                                                                                                                                                         DNA fragment encoding insecticidal protein - obtd. from Bacillus
thuringiensis sub species israelensis, and used in microorganisms
plant cells.
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TCAGCTGGGGGAATTTATCTAATGATAAAAAACAACTGATTTTCAATTTCCTGTAAAA
                                                GGAATACCACCTCAACGACTCAACACACTTTTTCTGGTACAAATTATAATAATTTACAA
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LysAspCysAsnLeuVallleAspProGlyCysSerProAsnPheAsnAsnTyrSerHis
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166 AsnThrGlnAspValArgThrGlnIleGlnLeuValHisTyrHisPheGlnAsnValIle 185
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375 ThrProAsnAsnPhePhe---ThrSerHisTyrAsnMetPheHisTyrThrLeuAspAsn
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394 IleSerGlnLysSerSerValPheGlyAsnHisAsnValThrAspLysLeuLysSerLeu
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AspvalValAlaLeuPheProAsnTyrAspValGlyLysTyrProlle------
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---ThrGlnValTyrThrPheAla----TrpThr
                                                                                               602 AlaValileAsnLeuSerileProGlyValAlaGluLeu---GlyMetAlaLeuAsnPro
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                                                                          CACAGTAGTGTTAATAGAAATAATGCAATATCAGATAAAATAATTACAATGATCCCAGCA
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expression cassette; transformation; transgenic; plant;
lepidopiera; coleoptera; pest; pesticide; resistance;
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20-FEB-2003; 2003US-0448633P.
20-FEB-2003; 2003US-04487P.
20-FEB-2003; 2003US-0448806P.
20-FEB-2003; 2003US-04488110P.
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                                                                                                                                                                                                                                                                                   This sequence represents a delta-endotoxin crystal protein. This protein was included in the scope of the invention as a comparison to the delta-endotoxins of the invention. Some of the delta-endotoxin oclain sequences of the invention have alternative start codons, producing more than one protein from a single open reading frame. The nucleic acid sequences of the invention are useful in DNA constructs or expression casesttes for transformation and expression in plants and bacteria. The nucleic acids and corresponding polypeptides are useful for killing lepidopteran or coleopteran pests. Compositions containing the delta-endotoxins of the invention, and methods for their production, are useful for the production of organisms with pesticide resistance, specifically bacteria and plants. These organisms are useful for generating altered or improved delta-endotoxin or nucleic acids in products or
                                                                                                                                                                                                 isolated delta-endotoxin and delta-endotoxin-associated nucleic acids polypeptides, useful for killing lepidopteran or coleopteran pests or producing organisms with pesticide resistance.
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|ThrValLeuThrGlyPheGlyPheThrThr------ProLeuGlyLeu
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2004US-00781979.
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19-FEB-2004; 2
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| AsnThr---TrpSerAspPheileThrGlnThrLysAsnIleIleLysLysGluileAla 130
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LysPheGluAlaTyrLeuLysAsnAsnAsGlnPheAspTyrLeuGluPro---LeuPro
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|IyAspLeuIle-----AspPheLysAspHisPheLysIleThrCysGlnHisSerAsn
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The protein is encoded by an insert in plasmid pCC130. The delta endotoxin protein is insecticidal and can be used to control insect pests esp; meaquitos. See also AAP93715. (Updated on 25-MAR-2003 to correct PAfield.) (Updated on 25-MAR-2003 to correct DR field.) (Updated on 27-MUG-2003 to correct OS field.)
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TyrHisAsnHisLeuLysThrTrpGlu------AsnAsnProAsnProGln 165
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SerThrTyrlleSerAsnAlaAsnLysIleLeuAsnArgSerPheAsnVallleSerThr
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thuringlensis sub species israelensis, and used in microorganisms and
plant cells.
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                               A plasmid contg. the gene is isolated by forming a gene library from plasmid DNA of B.thuringiensis israelensis (HD 522 strain, USA Goldberg ONRGO) followed by screening with anti-israelensis insecticidal protein IG. The insecticidal protein is highly effective against Diptera, esp. Aedes. See also AAP81034. (Updated on 24-OCT-2003 to standardise OS
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|TyrHisAsnHisLeuLysThrTrpGlu------AsnAsnProAsnProGln
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AsniysAsndluTyrdluThrLeuAsnAlaSerGlniysIysLeuAsn1leSerAsnAsn
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ProGluLeuValAgnSerCysProProAgnProSerAgpCygAgpTyrTyrAgnIleLeu
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Conservative:
Mismatches:
Indels:
Gaps:
acid,
plasmid deoxyribonucleic
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                Disclosure, Page ?; 9pp; Japanese.
                                                                                                              1.68e-88
1157.00
54.55%
37.29%
29.37%
                                                                                                                                       Similarity:
                                                                                       Sequence 1180 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTCACAAATCATACAAAAAATACTTTAAATATAGAAGCCACAAACTATGATATTGAT 2232
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AUG-2003 to correct OS field.)
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LysPheGluAlaTyrLeuLysAsnAsnArgGlnPheAspTyrLeuGluPro---LeuPro
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                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR63078 standard; protein; 1180 AA
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(first entry)
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                                                                                                           GATACTATCGCTCAATTTTTCTTTTATGATAAAGAGATACAAAGATTCAATAGGAAGA 1002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     471 LysasnilephedlyLeuProileLeuLysProargGluasnGlnalaileProThrLeu 490
                                     ---AATATGAGATGGAGTATATTAATGATTATCGAAGATATATGACTATTACTGTATTA 942
ValThrThrTyrLysLysGlyLeuAsnLeuIleLysThrThrProAspSerAsnLeuAsp 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    452 ArgLeuLeuGluLysGluLeuThr---AlaglySerGlyGlnIleThrTyrAspValAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ||||||| :::|||||| ||| 356 ArgPro---HisLeuPheThrTrpLeuAspSerLeuAsnPheTyrGluLysAlaGlnThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                      375 ThrProAsnAsnPhePhe---ThrSerHisTyrAsnMetPheHisTyrThrLeuAspAsn
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| HisSerSerValAspProLysAsnThrIleTyrThrHisLeuThrThrGlnIleProAla
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Delta-endotoxin, crystal protein, biological control agent, Calliphorid,
screw-worm, sheep blowfly, Lucilla, Phormia, Calliphora, insecticide;
                                                                                                                                                                                                                                                                                                                                                     2176 TICACAAATCATACAAAAATACTTTAAATATAGAAGCCACAAACTATGATATTGAT 2232
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641 SerAsnGluValLysPheAlaProAsnGlnAsnIleSerLeuValPheAsnArgSerAsp
                                                                                                                                                         2059 GTA---TCAAATTCAATTTTAATCATTGATAAAATTGAATTTATACCAATTACTTCCTCT
                                                                                                                                                                                       or controlling Calliphoridae pests - specifically utilises thuringiensis isolates or toxins.
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Conservative: Mismatches:

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Percent Similarity:
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                       661 ValTyrThrAsnThrThrValLeuIleAspLysIleGluPheLeuProIleThrArgSer 680
                                                                    ITCACAAATCATACAAAAATACTITIAAATATAGAAGCCACAAAACTATGATATTGAT 2232
                                                                                  Novel isolated delta-endotoxin nucleic acid molecules, cry26Aal and cry28Aal isolated from Bacillus thuringiensis finitimus, that encodes toxin active against insects, useful for controlling insects.
                                                                                                                                                                                                                                    Delta-endotóxin, cry26Aal; cry28Aal; insect-resistant plant; toxin;
transgenic host cell; insecticide.
                                                                                                                                                                                                              Bacillus thuringiensis ssp. finitimus cry28Aa1 delta-endotoxin.
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                                                                                                                                           AAE26353 standard; protein; 1109
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ZALUNIN I A.
REVINA L P.
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N-PSDB; AAD43974.
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Chestukhina GG;
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Alignment Scores: Pred. No.:

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LysGlulleAlaLeuAlaHisLeuAsnGlyPheLysAspValLeuThrTyrTyrGluArg 120
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|TyrAapGluLeuLeuValTyrileGluLysTyrileAsnTyrCysThriysThrTyrHis 225
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266 ArgArgPhePro------ArgGlyValGluLeuGluLeuThrArgGlu
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TrpAsnAlaAspGlnProHisSerProMetLeuLysSerSerGlyThr-----Tyr
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|SerSerAspThrValAlaValValSerAlaGlyIleValValValGlyThrIleLeuThr
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------AlaPheAlaSerPheValAsnPro------GlyValValLeuIle
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---LeuAspHisLeuThrArgProProGly---
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619 AsnValLeuPhelleAsnAlaThr -- - AsnAlaLeuLysMetAspValThrAspTyrHis
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                                                                                          336 Asn------ThrAsnArgLeuSerLysGlnLeuIleThrLeuLeuProGly 350
                                                                                                                                             351 Glu---PheMetThrHisLeuSerIleAsnArgProPheGlnThrIleAlaGlyIleAsn 369
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452 ValAsnSerGlnAsnLeulleSerGluSerValSerThrGlnIleProLeuValLysAla 471
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                                                                                                                                                                                      370 LysLeuTyrSerLeuileGlnLysile-----ValPheThrThrPheLysAsnAsp
317 ---ArgGluSerLysTyrTyrThrGlyAsnGlnPhePheThrMetLysAsnileTyrGly
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated nucleic acid molecule encoding a toxin that is active against insects useful for controlling insect pests or for conferring insect resistance in plants.
                                                                                                                                                                                                                                                                                                                                                                                  Bacillus thuringiensis serovar finitimus cry28Aa1 delta-endotoxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Cry26Aal; cry28Aal; delta-endotoxin; insect pest control;
transgenic plant; insect resistance; insecticide.
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                                                                                                                                                                                                                    ADF31302 standard; protein; 1109 AA
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CGGAGATTTTGGGTATTTC 1992 rccaaatrgrttaccaagc 1533 AATTGAATTTATACCAATT 2106 AGAAGCCACAAACTATGAT 2226
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tAspValThrAspTyrHis 637 TAATTCACCTAGTAATAAA 1422 TTTATTTATTTCCTAT 1587 AGGATGGACACACAGTAGT 1647 GATCCCAGCAATCAAAGGT 1707 |||||| nIleProLeuValLyBAla 471 AACTCCTAATTCTACACAA 1827 AAATACTCTTCCTAATATA 1887 ACTCAACACTTTTTCT 1947 ACCATTTATATTTAATCGT 2052 AACTATCCAAACAAAATA 2166 eHislleHisLeuLysArg 581 ::: eThrThrPheLysAsnAsp 386 ||||||| -ProAsnAspTyrGlyGly 413 : :::||| ::: sAla---SerSerLeuLys 507 -LeuGlnProThrPheSer 541 | ::: :: :: uLysAlaLysLysAlaVal 618 ::: nThrileAlaGlyIleAsn 369 |||| obeullelleHisbysbeu 433 eAlaValSerIleAspVal 527

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976 AAGAGATACAAAGATTCAATAGGAAGAATAGGTGGCATTAAAACTGAACTTACAAGAGAA 1035
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LysGluIleAlaLeuAlaHisLeuAsnGlyPheLysAspValLeuThrTyrTyrGluArg
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                                                           GCATTAGATGATTGGAGAAAATTAAAAAGACTACAAGCTCCTGGATTACCACCATCATCA
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266 ArgArgPhePro-------ArgGlyValGluLeuGluLeuThrArgGlu
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|SerSerAspThrValAlavalValSerAlaGlyIleValValValGlyThrIleLeuThr 47
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGTGCTGATACAATTGCTGCAGTTAGTGCAGGTACTATTGTATCCGGTACTCTGTTAGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              delta-endotoxin nucleic acid molecules, cry26Aa1 and cry28Aa1, controlling insect pests and for conferring insect resistance.
                                 Bacillus thuringiensis serovar finitimus cry28Aal delta-endotoxin.
                                                                       Cry26Aa1; cry28Aa1; delta-endotoxin; insect pest control.
transgenic plant; insect resistance; insecticide.
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                                                                                                                                 Bacillus thuringiensis serovar finitimus
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LEWITIN E I.
ZALUNIN I A.
REVINA L P.
(first entry)
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                                                                                                      ValAsnSerGlnAsnLeuileSerGluSerValSerThrGlnileProLeuValLysAla 471
                                                                                                                                                                                                                                                                                                                                                                                                                        Tyr-----ProAsnAspTyrGlyGly 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Delta-endotoxin, crystal protein; biological control agent; Calliphorid; screw-worm; sheep blowfly; Lucilla; Phormia; Calliphora; insecticide; pesticide; B.t.
                                                  GTTAATAGAAATAAGCAATATCAGATAAAATAATTACAATGATCCCAGCAATCAAAGGT
                                                                                                                                                                      ::: |||::: :::||| ::: ||| | | ||::: :::||| ::: IleGluLeuArgAsp-----LysCysSerIleLysCysLysAla---SerSerLeuLys
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528 GlyAspSerGlyAlaGlyValLeu--------LeuGlnProThrPheSer
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                                                                                                                         AACAGTCTTGATACAAACTCTAAGGTAATTGAAGGACCTGGTCATACAGGAGGAAACTTG
                                                                                                                                                           GTTTATTTTACAAAGTCAAGGGCGTTTAGAGATTACATGTAGAACTCCTAATTCTACAAA
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A library was constructed from Bacillus thuringlensis PS71M3 total cellular DNA in lambda Gem-11. Plasmid pMYC1636, selected in Escherichia coli, contained a 15 kb insert expressing a beta-endotoxin gene. This was sequenced (AAQ81180). A cured, acrystalliferous B.t. host carrying pMYC1636 produced a 77 kba crystall protein (AAR63079). (Updated on 25-MAR-2003 to correct PN field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TTAGCCGGTATAGGTGGGCTCACTTCTATATCCGGACCGATAGGAATAATAGGTGCTATA 312
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                                                                                                                                                                                                                                                                        Method for controlling Calliphoridae pests - specifically utilises Bacillus thuringiensis isolates or toxins.
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13-JUL-1994;
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|ValTrpGlnAspLeuLeuAsnIleGly------GlyArgProlleGlnGluIle 130
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| 131 AspLysAsnIlelleAsnValLeuThrSerIleValThrProIleLysAsnGlnLeuAsp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                604 CACAAT-----GATTTTATTCGAGAAATACCTGGTTTCCAACTTGAAACTTATAAA 654
                                                                                                                          The sequence was deduced from the DNA sequence obtd. from plasmid pMYCL636 which was isolated from a genomic library prepd. from DNA from B.t. PS71M3-69 (NRRL B-18515)]. It is related to the crylVC toxins from B.t. var. israelensis. The protein has a mol. wt. of dipteran insects or their environ-ments, the expressed toxins acting as an insecticide. See also AAAI4373. (Updated on 25-MAR-2003 to correct PA field.) (Updated on 27-MUG-2003 to correct PA field.)
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                                                               Bacillus thuringiensis genes encoding diptera-active toxins - and transformed microbes used to control insects in various environments
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1437 1318 TCAATTGTAACTGATAGACAAGTAACTCCCTACTTCCCCTTTTCCTAACATATACTTTACA 1377 GCTCAATTTTTTTTATGATATAAAGAGATACAAAGATTCAATAGGAAGAATAGGTGGC 1011 1618 ACAGGTGCATTAGGATGGACACACAGTAGTGTTAATAGAAATAATGCAATATCAGATAAA 1677 412 471 831 891 951 |||::::::::||| ||||||| ThrTrpAsnMetTyrAspLeuIle 293 AACTATTGTGCAAATACCTATAGAGAAGGACTAAATAAACTTCGAAACGAACCTAATATG ::: ||| 360 AspProTyrAspIlePheSerPheThrGlyAsnGlnMetAla-------GGTGCTGAATTGGCTGATGGAATGCAGATATACATCCTTCACAATTGAACCTAAT GCTGGAACATCAGATGACTATTATAAA---CTTTTAAAAGAAAATATACCTAAATATAGT AsplyrCyslleGlnThrTyrAsnAlaGlyLeuThrMetlleArgThrAsnThrAsnAla AGATGGAGTATATTAATGATTATCGAAGATATATGACTATTACTGTATTAGATACTATC ---PherhrhisThrAsnAspAspArgAsnileileTrpGlyAlaValHisGlyHisIle ---CCACCCACACAAAAACTTTAATACCATTTGAATCCTAT------AAAGTT GluilevalArgHisArgGlu------TyrSerAsp 1378 ATTAATCAAATTGAACTTTATTTAAATAATTCACCTAGTAATAAATTAACATATTCAGCT GGGGGGAATTTATCTAATGATAAAAAAACAACTGATTTTCAATTTCCTGTAAAAAAAGAC AsnSerThrIleGluAsnAsnTyrLysArgThrAspSerTyrMetIleProLysGlnThr TGTAAACCAATTATTAATCCAAATTGTTTACCAAGCTATAATAGTTATAGTCATATTTTA **ACGCTATTACTACCTATTTATGCGCAAGCTGCTAATTTTCATTTAAATTTATTACAACAA** AlaalaThrTyrTyrAsnIleTrp-----LeuGlnAsnGlnGlyileAsnProSer ThrPheAsnSerSerAsnTyrTyrGlnGlyTyrLeuLysArgLysIleGlnGluTyrThr AlailepheProAsnTyrAspProGluLysTyrProIle-------Gly AGATTATTTTCATTTTTAGATGAACTTATATTTTTATACAAAAAT--------TACCTTGAAATTCAACCCAATCTCGCTATAATGGAATATATTTAACACGTTCAGGGCTT ::: ||| :::::: ||| Ilaspiration

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ArgValAlaPheSerTrpThrHisThrSerValAspPheGlnAsnThrIleAspLeuAsp 508
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               1678 ATAATTACAATGATCCCAGCAATCAAAGGTAACAGTCTTGATACAAACTCTAAGGTAATT
                         ThriyralaAspPheGlyTyrValThrPheProArgThrValProAsnLysThrPheGlu
                                                                                                                                                                                                                                                               |||| :::||| SerTyrAsnIle---TyrIleAspLysIleGluPheIleProIleThrGlnSerValLeu
                                                 GAAGGACCTGGTCATACAGGAGGAAACTTGGTTTATTTACAAAGTCAAGGGCGTTTAGAG
                                                                                 1798 ATTACATGTAGA---ACTCCTAATTCTACACAATCTTATTACATTAGACTTCGATACGCT
                                                                                             |||| :::|||| :::||| PheArgValArgGlnTyrGlnValArgIleArgTyrAla
                                                                                                                              ATACCACCTCAACGACTCAACAACTTTTTCTGGTACAAATTATAAT-----AATTTA
                                                                                                                                                                                   CAATACGGAGATTTTGGGTATTTCCAAGTACAGTA-----
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                                                                                                                                                                                                                                    GlyGluAspThrLeuLeuMetThr-------LeuTyrGlyThrProAsnHis
                                                                                                                                                                                                                                                     TCAAATTCAATTTTAATCATTGATAAAATTGAATTTATACCAATTACTTCCTCTGTACGC
                                                                                                                                                                                                                                                                                     delta-endotoxin; delta-endotoxin associate polypeptide;
expression cassette; transformation; transgenic; plant; bacteria;
lepidoptera; coleoptera; pest; pesticide; resistance;
                                                                                                                                                                                                                                                                                                                                                                     ADR89431 standard; protein; 675 AA
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2003US-0448797P.
2003US-0448810P.
2003US-0448812P.
2004US-00781979.
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20-FBB-2003;
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20-FBB-2004;
19-FBB-2004;
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This sequence represents a delta-endotoxin crystal protein. This protein was included in the scope of the invention as a comparison to the delta-endotoxins of the invention. Some of the delta-endotoxin coding sequences of the invention aver alternative start codons, producing more than one protein from a single open reading frame. The nucleic acid sequences of the invention are useful in DNA constructs or expression cassettes for transformation and expression in plants and bacteria. The nucleic acids and corresponding polypeptides are useful for killing lepidopteran or coleopteran pests. Compositions containing the delta-endotoxins of the invention, and methods for their posticide resistance, specifically bacteria production of organisms with pesticide resistance, specifically bacteria and plants. These organisms are useful for generating altered or improved delta-endotoxin or delta-endotoxin are useful for senerating altered or improved delta-endotoxin or delta-endotoxin-associated proteins that have
                                                                                                                                                                                                                                                                                                                                    New isolated delta-endotoxin and delta-endotoxin-associated nucleic acids and polypeptides, useful for killing lepidopteran or coleopteran pests or for producing organisms with pesticide resistance.
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TyrLygAspTrpLeuAsnValCysGlnAspAsnGlnGlnTyrGlyAsnAsnAlaGlyAsn
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Matches:
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                                                                                                                                                                                                                     Koziel MG,
19-FEB-2004; 2004US-00782096.
19-FEB-2004; 2004US-0078141.
19-FEB-2004; 2004US-00783570.
19-FEB-2004; 2004US-00783417.
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qq	131	::: ApplysAsnilelleAsnValLeuThrSexileValThrProlleLysAsnGlnLeuAsp 150	
à	484	AGCTATAATACAGCATTAGATGATTGGAGAAAATTAAAAGACTACAAGCTCCTGGATTA 543	
QQ Q	151	LysTyrGlnGluPhePheAspLysTrpGluProAlaArg163	
ò	544	CCACCATCATCAGCATTACAACAAGGGGCCTTGACTATAAATACGATTTGAGAATGTT 603	
g G	164	ThrHisAlaAsnAlaLysAlaValHisAspLeuPheThrThrLeuGluProlle 181	
ò	604	CACAATGATTTTATTCGAGAAATACCTGGTTTCCAACTTGAAACTTATAAA 654	
QQ	182	IleaspiysaspieuaspmetieulysasnasnalaserTyrargileProThr 199	
ò	655	ACGCTATTACTACCTATTTATGCGCAAGCTGCTAATTTTCATTTAAATTTATACAACAA 714	
QQ	200	LeuProalaTyralaGinilealaThrTrpHisLeuAsnLeuLeuLysHis 216	
č	715	GGIGCTGAAITGGCTGATGAATGCAGATATACATCCTTCACAAATTGAACCTAAT 774	
Q Q	217	AlaalaThrTyrTyrAsnIleTrpLeuGlnAsnGlnGlyileAsnProSer 233	
è	775	GCTGGAACATCAGATGACTATTATAAACTTTTAAAAGAAAATATACCTAAATATAGT 831	
qq	234	ThrPheAsnSerSerAsnTyrTyrGlnGlyTyrLeuLysArgLys1leGlnGluTyrThr 253	
à	832	AACTATTGTGCAAATACCTATAGAGAAGAACTAAATAAACTTCGAAACGAACCTAATATG 891	
qq	254	**: AspTyrCysileGlnThrTyrAsnAlaGlyLeuThrMetIleArgThrAsnThrAsnAla 273	
à	892	AGAIGGAGTATATTTAANGATTATCGAAGATATATGACTATTACTGTATTAGATACTATC 951	
QC QC	274	ThrTrpAsnMetTyrAsnThrTyrArgLeuGluMetThrLeuThrValLeuAspLeuIle 293	
È	952	GCTCAATTTTTTTTTTTATGATATAAGAGATACAAAGATTCAATAGGAAGAATAGGTGGC 1011	
qq	294		
È	1012	ATTAAAACTGAACTTACAAGAGAAATTTATACAACTGAAATAAAT	
QC QC	308	vallysSerGluLeulleArgGluValTyrThrAsnValAsnSerAspThrPheArg 326	
È	1072	TACCITGAAAITCAACCCAAICTCGCIAIAAIGGAAIAIAATITIAACACGTICAGGCCIT 1131	
qq	327	ThrileThrGluLeuGluAsnGlyLeuThrArgAsnPro 339	
È	1132	AGATTATTTTCATTTTTAGAACTTATATTTTTATACAAAAAAT 1176	
D p	340	ThrLeuPheThrTrpIleAsnGlnGlyArgPheTyrThrArgAsnSerArgAspIleLeu 359	
è	1177	GAAACGTACGGGAATCGTTTAGTTGGTATTGCGAATCGTAAT 1218	
qq	360	:::	
è	1219	AGATCTACTATGCTACGACAGGAACTGAAATTATATATGGAGAAAGAA	
ą a	374	PheThrHisThrAsnAspAspArgAsnIleIleTrpGlyAlaValHisGlyAsnIle 392	
è	1273	CCACCCACAAAAACTTTAATACCATTTGAATCCTATAAAGTT 1317	
q	393	IleSerGlnAspThrSerLysValPheProPheTyrArgAsnLysProlleAspLysVal 412	
È	1318	TCAAITGIAACTGAIAGACAAGIAACTCCTACTTCCCTATTCCTAACAIATACTTTACA 1377	
qq	413	GluileValargHisArgGluTyrSerAsp 422	
ò	1378	378 ATTAATCAAATTGAACTTTATTTAAATAATTCACCTAGTAATAAATTAACATATTCAGCT 1437	
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Squence 2, Application US/10782570

GENERAL INFORMATION:
APPLICANT: Carozai, Nadine
APPLICANT: Carozai, Nadine
APPLICANT: Carozai, Micholas B.
APPLICANT: Cari, Micholas B.
APPLICANT: Cari, Brian
TITLE OF INVENTION: Methods for Its Use
FILE REPERRENCE: 045600/274144
CURRENT APPLICATION NUMBER: US/10/782,570
CURRENT FILING DATE: 2004-02-19
PRIOR APPLICATION NUMBER: 60/448,812
PRIOR PELICATION NUMBER: 60/448,812
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Mismatches:
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US-10-782-096-18

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US-10-783-570-14

US-10-783-91-19

US-10-781-919-19

US-10-926-819-16

US-10-929-754-1

US-10-782-914-4

US-10-782-914-4

US-10-782-914-2

US-10-782-912-1

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SOFTWARE: FastSEQ for Windows Version 4.0
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LENGTH: 744
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3: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
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	241 TCCGGTACTCTGTTAGCCGGTATAGGTGGGCTCACTTCTATATCCGGACCGATAGGAATA 241 TCCGGTACTCTGTTAGCCGGTATAGGTGGGCTCACTTCTATATCCGGACCGATAGGAATA 81 SerGlyThrLeuLeuAlaGlyIleGlyGlyCeuThrSerIleSerGlyProileGlyIle	301 ATAGGTGCTATAATATTCTTTTGGTACCCTAATCACTGTCTTTTGGCCGGGGGGAAA 101 IleGlyAlaIleIleIleSerPheGlyThrLeuIleThrValPheTrpProAlaGlyGlu 361 CAAGACAAAAGAGTATGGACACAATTTATTAAAATGGGAGAAATTTTTGTTGATGACCG	121 GlideplysThrValTrpThrGlinPhelleLysMetGlyGluilePheValdspphrPro 421 TTAACAGAAAGCATAAAACAGCTAAAGTTACAAACTTTAGAAGATTAGACAATTTAGACAATTTAGACAATTTAGACAATTTAGACAATTTAGACAATTTAGACAATTTAGACAATTTAGACAATTTAGACAATTTAGACAATTTAGACAATTTAGACAATTTAGACAATTTAGACAATTTAGACAATTAGACAATTAGACAATTAGACAATTAGACAATTAGACAATTAGACAATTAGACAATTAGACAATTAGACAATTAGACAATTAGACAATTAGACAATTAGACAATTAGACAATTAGACAATTAGACAATTAGACAATTAGACAATAGAATAGACAATAGA	CAAGCTAATAATACAGCATTAGTGATGAGGAAAATTAAAAAGACTACAGGTC	541 TTACCACCATCACATTACAACAAGCTGCCTTGACTCTTAAAATACGATTTGAGAAT	601 GTTCACAATGATTTTATTCGAGAAATACCTGGTTTCCAACTTGAAACTTATAAACGCTA	TTACTACCTATTTATGCGCAAGCTGCTAATTTTCATTTAAATTTATTACAAAG 	721 GAATTGGCTGATGGAATGCAGATATACATCCTTCACAAATTGAACCTAATGCTGGA 	ACATCAGATGACTATTATAAACTTTTTAAAAGAAATATACCTAAATATAGTAACT 	841 GCAAATACCTATAGAGAAGGACTAAATAAACTTCGAAACGAACCTAATATGAGATGGAGT [ATATITAATGATTATCGAAGAATATGACTATTACTGTATTAGATACTATGCCTC		

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                                                 US-10-102-20-0-4
Sequence 4, Application US/10782570
Sequence 4, Application US/2040210955A1
GENERAL INFORMATION:
APPLICANT: Carozzi, Nadine
APPLICANT: Hardiss, Tracy
APPLICANT: Carozzi, Michael G.
APPLICANT: Carr, Brian
TITLE OF INVENTION: Methods for Its Use
TITLE OF INVENTION: Methods for Its Use
FILE REFERENCE: 045600/27414
CURRENT FILING DATE: 2004-02-19
PRIOR APPLICATION NUMBER: 05/448,812
PRIOR PLICATION NUMBER: 60/448,812
PRIOR PLICATION NUMBER: 60/448,812
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 694
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Matches:
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                     CGTTTAGTTGGTATTGCGAATCGTAATAGATCTACTTATGCTACGACAGGAACTGAAATT 1251
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RESULT 4 US-10-782-141-12

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166 AsnThrGlnAspValArgThrGlnIleGlnLeuValHisTyrHisPheGlnAsnVallle 185
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Publication No. US20040197917A1

GENERAL INNORMATION:
APPLICANT: Carczzi, Nadine
APPLICANT: Hargiss, Tracy
APPLICANT: Carczzi, Nacholas B.
APPLICANT: Carc, Micholas B.
APPLICANT: Carr, Brian
TITLE OF INVENTION: Methods for Its Use
TITLE OF INVENTION: Methods for Its Use
TITLE OF INVENTION: Methods for 12004020
TITLE OF INVENTION: Methods for 12004020
TITLE OF INVENTION: Methods for 12004020
FILE REPERENCE: 020040220
CURRENT FILING DATE: 2004-02-20
PRIOR PILING DATE: 2003-02-20
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12
LEMOTH: 1180
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uGluLysGluLeuThr---AlaGlySerGlyGlnIleThrTyrAspValAsn 470 |::: nule-----AspPheLysAspHisPheLysIleThrCysGlnHisSerAsn 581 :::||||| rLys------ThrGlnValTyrThrPheAla-----TrpThr ||| :::||||||||| odyrLysTyr-----AspPheGlnTyrGlnGluAspSerLeuThrArg | :::::: |||| nAsnPhePhe---ThrSerHisTyrAsnMetPheHisTyrThrLeuAspAsn

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| AsnThr---TrpSerAspPhelleThrGlnThrLysAsnIleIleLysLysGlulleAla 130
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| AsnlysAsnGluTyrGluThrLeuAsnAlaSerGlnLysLysLeuAsnIleSerAsnAsn 25
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                              TTCACAAATCATACAAAAATACTTTAAATATAGAAGCCACAAAACTATGATATTGAT 2232
                                         GAGACATTTGCTAGTGCTGATACAATTGCTGCAGTTAGTGCAGGTACTATTGTATCCGGT
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                                                                                       Sequence 10, Application US/10782570
Sequence 10, Application US/10782570
Sequence 10, Application US/10782570
Sequence 10, Application No. US20040210965A1
GENERAL INFORMATION:
APPLICANT: Carozat, Nadine
APPLICANT: Koziel, Michael G.
APPLICANT: Carr, Brian
TITLE OF INVENTION: Abvil-007, A Delta-Endotoxin Gene and
TITLE OF INVENTION: Methods E.
TITLE OF INVENTION: Methods for Its Use
FILE REFERENCE: 045600/274144
CURRENT APPLICATION NUMBER: 08/10/782,570
CURRENT FILING DATE: 2003-02-19
PRIOR APPLICATION NUMBER: 60/448,812
PRIOR FILING DATE: 2003-02-20
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PRESENCE of Windows Version 4.0
SEQ ID NO 10
LENGTH: 1180
TYPE: PRI
ORAMISM: Bacillus thuringiensis
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Matches:
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186 ProgluLeuValAsnSerCysProProAsnProSerAspCysAspTyrTyrAsnIleLeu
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TATAATACAGCATTAGATGATTGGAGAAAATTAAAAAGACTACAAGCTCCTGGATTACCA
                                      151 TyrHisAsnHisLeuLysThrTrpGlu------AsnAsnProAsnProGln
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|HisSerSerValAspProLysAsnThrIleTyrThrHisLeuThrThrGlnIleProAla
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Publication No. US20040216186A1
GENERAL INFORMATION:
APPLICANT: Carcozi, Nadine
APPLICANT: Koziel, Michael G.
APPLICANT: Duck, Nicholas B.
APPLICANT: Duck, Nicholas B.
APPLICANT: Carr, Brian
TITLE OF INVENTION: Axmi-006, A Delta-Endotoxin Gene and
TITLE OF INVENTION: Methods for Its Use
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CURRENT APPLICATION NUMBER: US/10/783,417

CURRENT FILING DATE: 2004-02-20

FRIOR APPLICATION NUMBER: 60/448,806

FRIOR FILING DATE: 2003-02-20

NUMBER OF SEQ ID NOS: 15

SOFTWARE: FBSEESQ for Windows Version 4.0

SEQ ID NO 8

LENGTH: 1180
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; ORGANISM: Bacillus thuringlensis
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166 AsnThrGlnAspValArgThrGlnIleGlnLeuValHisTyrHisPheGlnAsnValIle 185
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    Length:
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0999 CCAAGTACAGTAACATTACCTTTAAATCGAAACATACCCCAAGACTACCCCAAGACATACCTTTAAATCGAAAATTGACATACAT	RESULT 8 US-10-781-979-14 i Sequence 14, Application US/10781979 i Publication No. US20040250311A1 i GENERAL INFORMATION: APPLICANT: Carcazi, Nachael G. APPLICANT: Raziel, Michael G. APPLICANT: Duck, Nicholas B. APPLICANT: Cart. Brian i TITLE OF INVENTION: Methods for Its Use TITLE OF INVENTION: Methods for Its Use TITLE OF INVENTION: Methods for 15 Use TITLE OF INVENTION: Methods for 15 Use FILE REFERENCE: 04560/274147 CURRENT APPLICATION NUMBER: 405/10/781,979 PRIOR FILING DATE: 2004-02-20 NUMBER OF SEQ ID NOS: 28 SOFTMARE: FasteSEQ for Windows Version 4.0 SEQ ID NO 14 LENGTH: 1180 TYPE: PRT TYPE: PRT TYPE: PRT SEQ ID NO 14 LENGTH: 1180 TYPE: PRT TYPE: PRT US-10-793-19-14	Alignment Scores: 7.86e-87 Length: Fred. No.: 7.86e-87 Length: Score: 1158.00 Matches: Fercent Similarity: 54.55\$ Conservative: Best Local Similarity: 37.29\$ Mismatches: Ouery Match: 5.940\$ Gaps: BB: 5.40\$ Gaps:	- 78 0 1	Db 187 ACTION TRANSPORTS OF THE ACTION TO TH
943 GATACTATCGATTTTCTTTTTATGATATAAGGATACAAAGATTCAATAGGAAGA 1002		1525 TTACCAAGCTATAATAGTTATAGTCATATTTTATCCCAGTTTTCTTTAATTAT 1581 491 PheProThrTyrAspanTyrSerHisIleLeuSerPheIleLysSerLeuSerIlePro 510 1582TCCTATAAAATTGGATTAGCGCTAAATATATTATATACAGGTGCATTAGGATGGACA 1638 1581 AlaThrTyrLysThrGlnValTyrThrPheAlaTrpThr 523 1639 CACAGTAGTGTTAATAGAAATAATGCAATATCAGATAACAATAACAATGATCCCAGCA 1698		
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|AsnThr---TrpSerAspPhelleThrGlnThrLysAsnIleIleLysLysGluIleAla 130
                                                                                                                                                              TyrHisAsnHisLeuLysThrTrpGlu------AsnAsnProAsnProGln 165
---AlaLeuIleGlyPheGlyThrLeuIleProValLeuPheProAlaGlnAspGlnSer 111
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LysTyrLeuAsnAspTyrAsnAsnIleSerLysMetAspPhePheIleThrAsnGlyThr
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394 IleSerGlnLysSerSerValPhedlyAsnHisAsnValThrAspLysLeuLysSerLeu
                                                                                                  SerThrTyrlleSerAsnAlaAsnLysIleLeuAsnArgSerPheAsnVallleSerThr
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-----GlyLeuAlaThrAsn1leTyr1lePheLeuLeuAsnVal11eSerLeuAspAsn
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LysPheGluAlaTyrLeuLysAsnAsnArgGlnPheAspTyrLeuGluFro---LeuPro
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Sequence 4, Application US/09756526A

Sequence 4, Application US/09756526A

Patent No. US20020038005A1

GENERAL INFORMATION:
APPLICANT: Byogen, Lewitin
APPLICANT: Evgeny, Lewitin
APPLICANT: Galunin
APPLICANTON UNMBER: US/09/756,526A
CURRENT PILING DATE: 2001-01-08
PRIOR FILING DATE: 2000-01-07
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                                                                        471 LysAsnIlePheGlyLeuProlleLeuLysArgArgGluAsnGlnGlyAsnProThrLeu
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GlyaspLeulle----AspPheLysAspHisPheLysIleThrCysGlnHisSerAsn
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                                                                                                                                                   ---TCCTATAAAATTGGATTAGCGCTAAATATATATATATACAGGTGCATTAGGATGGACA
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--AGTAATAAATTAACATATTCAGCTGGGGGGAATTTATCTAATGATAAAAA
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                 1036 ATTTATACAACTGAAATAAATTTTGACCGTCTTACTTTACCTTGAAATTCAACCCAATCTC 1095
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-----LeuAspHisLeuThrArgProProGly---
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---ArgGluSerLysTyrThrGlyAsnGlnPhePheThrMetLysAsnIleTyrGly
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                                                                      GCTATAATGGAATATAAATTTAACACGTTCAGGGCTTAGATTATTTTTTAGATGAA
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TrpSerGlnPheMetLysHisGlyGluAspLeuLeuAsnGlnThrIleSerThrAlaVal 100
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LysGluIleAlaLeuAlaHisLeuAsnGlyPheLysAspValLeuThrTyrTyrGluArg 120
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ArgArgPhePro------ArgGlyValGluLeuGluLeuThrArgGlu 279
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|SerSerAspThrValAlaValValSerAlaGlyIleValValValValGlyThrIleLeuThr
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240
106
242
114
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Matches:
Conservative:
Mismatches:
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                   GCALTACAACAAGCTGCCTTGACTCTTAAAATACGATTTGAGAATGTTCACAATGATTTT
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| Publication No. US20030150018A1
| GENERAL INFORMATION:
| APPLICANT: Jana, Wojciechowska |
| APPLICANT: Event |
| APPLICANT: Ludmila, Revina |
| APPLICANT: Ludmila, Revina |
| APPLICANT: Ludmila, Revina |
| APPLICANT: Galunin |
| APPLICANT: Galunin |
| APPLICANT: Ludmila, Revina |
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| APPLICANT: Logor, Zalunin |
| APPLICANT: Galunin |
| APPLICANT: Logor, Zalunin |
| APPLICANT: 
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602 AgpGluAgnTyr-----ThrAgnGluMetAgnLeuGluLygAlaLygLygAlaVal
GCAGAT-----GTATCAAATTCAATTTTAATCATTGATAAAATTGAATTTATACCAATT
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|SerSerAspThrValAlavalValSerAlad]y||evalValValValGjyThrIleLeuThr
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      Length:
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Publication No. US20030154510A1

GENERAL INFORMATION:

APPLICANT: Bryeny, Lewitin

APPLICANT: Evgeny, Lewitin

APPLICANT: Ludmila, Revina

APPLICANT: Gallua, Revina

APPLICANT: Lower Date: 2000-01-15

FILE REFERENCE: 2000-01-07

CURRENT FILING DATE: 2000-01-07

NUMBER OF SEQ ID NOS: 5

SOFTWARE: Patentin version 3.0
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                                                                                                                                 Sequence 17, Application US/10782141

Publication No. US20040197917A1

GENERAL INPORMATION:

APPLICANT: Carcazi, Nadine

APPLICANT: Hargiss, Tracy
APPLICANT: Carziel, Michael G.

APPLICANT: Carziel, Michael G.

APPLICANT: Carr, Brian

TITLE OF INVENTION: AXMI-014, A Delta-Endoton

TITLE OF INVENTION: Methods for Its Use
FILE REPERENCE: 045600/274443

CURRENT APPLICATION NUMBER: US/10/782,141

CURRENT APPLICATION NUMBER: 60/448,632

PRIOR PILING DATE: 2003-02-20

PRIOR FILING DATE: 2003-02-20

NUMBER OF SEQ ID NOS: 23

SEQ ID NO 17
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TYPE: PRT
ORGANISM: Bacillus thuringiensis
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Asn-----ThrAsnArgLeuSerLysGlnLeuIleThrLeuLeuProGly 350
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                                                                               iii | | | | | | | 407 Tyr------ProAsnAspTyrGlyGly
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LysTyrAlaileSerLeuPheTyrAlaAlaAsnAsnAlaileAlaValSerIleAspVal
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                                                             AATAGATCTACTTATGCTACGACAGGAACTGAAATT------ATATATGGA
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AGAAAATTAAAAAGACTACAAGCTCCTGGATTA GluProalaArg	775 GCTGGAACATCAGATGACTATTATAAA	AAAGAACAGGTi- lavalHisGlyAsnIleAAAGTT ysProIleAspLysVal CTAACATATACTTTACATyrSerAsp AATTAACATATTCAGCT
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APPLICANT: Hargiss, Tracy
APPLICANT: Koziel, Michael G.
APPLICANT: Koziel, Michael G.
APPLICANT: Duck, Nicholas B.
APPLICANT: Duck, Nicholas B.
APPLICANT: Cart. Brian
TITLE OP INVENTION: AMI-006, A Delta-Endotoxin Gene and
TITLE OP INVENTION: AMI-006, A Delta-Endotoxin Gene and
TITLE OP INVENTION: MICHAEL US/10/783,417
TITLE OP INVENTION: MUMBER: 60/448,806
RICH FILING DATE: 2003-02-20
RICH PLING DATE: 2003-02-20
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PastSEQ for Windows Version 4.0
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RESULT 15 US-10-783-417-12 Sequence 12, Application US/10783417 ; Publication No. US20040216186A1

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-	ACGCTATTACTACCTATTTATGCGCAAGCTGCTAATTTTCATTTAAATTTATTACAACAA 71.		GCTGGAACATCAGATGACTATTATAAACTTTTAAAAGAAAATATACCTAAATATAGT 831 ThrPheAsnSerSerAsnTyrTyrGlnGlyTyrLeuLy8ArgLys1leGlnGluTyrThr 253	AACTATTGTGCAAATACCTATAGAGAAGGACTAAATAAACTTCGAAACGAACCTAATATG 891 A8pIyrCysileGlnThrTyrAsnalaGlyLeuThrMet11eArgThrAsnThrAsnala 273	AGATGGAGTATATTAATGATTATCGAAGATATATGACTATTACTGTATTAGATACTATC 951	GCTCAAITTICTITITIAIGAIAAIAAAGAGAIACAAAGAITCAAIAGGAAGAATAGGIGGC 101 	ATTAAAACTGAACTTACAAGAGAATTTATACAACTGAAATAAAT	TACCTTGAAATTCAACCCAATCTCGCTATAATGGAATATAAATTTAACACGTTCAGGGCTT 113	AGATTATTTTTTTTTTAGATGAACTTATATTTTATACAAAAAAT	GAAACGTAC	AGATCTACTTATGCTACGACAGGACTGAAATTATATATGGAGAAGAAGGACGGT 127; 	E4	TCAAITGIAACTGAIAGACAAGTAACTCCCTACTTCCCCTTTTCCTAACATATACTTTACA 1377 ullevalargHisArgGlu	AITAATCAAAITGAACTITAITIAAAIAAITCACCIAGIAAIAAAITAACAIAITCAGCT 1437 	GGGGGGAATTTATCTAATGATAAAAACAACTGATTTTCAATTTCCTGTAAAAAAGAC 1497 ::: ::: AsnSerThrIleGluAsnAsnTyrLysArgThrAspSerTyrMetIleProLysGlnThr 461	1 4	TCCCAGTTTTCTTTATTTAATTACTATAAAATTGGATTAGGCTAAATATATAT	ACAGGTGCATTAGGATGGACACACAGTAGTGTTAATAGAAATATGCAATATCAGATAAA 1677
182 1	655 #	715 G 217 A	775 G 234 T	832 A 3 254 A	892 A 274 T	952 G 294 A	1012 A : 308 V	1072 T	1132 A 340 T	1177 G : 360 A	1219 A 374 -	1273 - 393 I	1318 T 413 G	1378 A 	1438 G 442 A	1498 T 462 T	1558 T	1618 A

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1969 CAATACGGAGATTTTTGGGTATTTCCAATTTCCAAGTACAGTA------ 2010
1678 ATAATTACAATCAATCCAGCAATCAAAGGTAACAGTCTTGATACAAACTCTAAGGTAATT 1737
509 ASNI16ThrGlnIleHisAlaLeuLysAlaLeuLysValSerSerAspSerLysIleVal 528
                                                                                                      1798 ATTACATGTAGA---ACTCCTAATTCTACAATCTTATTACATTAGACTTCGATACGCT 1854
                                                                                                                                                         1855 ACAAATGGTGCTGGAAATACTCTTCCTAATATGTCTTTACAATACCAGGAGTAATAGGA 1914
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567 ThrAsnAla-------ProLysThrThrValPheLeuThrGly1leAspThr 581
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Search completed: January 12, 2006, 06:39:43 Job time : 196 secs

12, Appl 114, Appl 120, Appl 220, Appl 221, Appl 221, Appl 121, Appl 122, Appl 123, Appl 124, Appl 124, Appl 124, Appl 124, Appl 125, Appl 126, Appl 126, Appl 126, Appl 127, Appl 128, Appl 129, Appl 120, Appl 120, Appl 131, Ap

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MAPLICANT: Ronald D. Flannagan

APPLICANT: Rafael Herrmann

APPLICANT: Rafael Herrmann

APPLICANT: Theodore W. Kahn

APPLICANT: Theodore W. Kahn

APPLICANT: James K. Presnail

APPLICANT: James K. Presnail

APPLICANT: James F. H. Wong

APPLICANT: Cao-Guo Yu

APPLICANT: Cao-Guo Yu

TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal

FILE REFERENCE: 35718/287809

CURRENT APPLICATION NUMBER: 60/131, 786

PRIOR PILING DATE: 2003-06-02-15

PRIOR PILING DATE: 2003-06-04

PRIOR PILING DATE: 2003-06-04

PRIOR PILING DATE: 2003-06-04

PRIOR PILING DATE: 2003-06-05

SEQ ID NOS: 134

SEQ ID NOS: 134

SEQ ID NOS: 134

TENDER OF SEQ ID NOS: 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-11-058-727-4; Sequence 4, Application US/11058727; Publication No. US20050261483A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Bacillus thuringiensis
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1: /cgn2 6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

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Copyright (c) 1993 - 2006 Compugen Ltd
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US-11-108-389-4
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US-11-1058-72-2
US-11-192-801-5
US-11-192-801-2
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Maximum Match 100%
Listing first 45 summaries
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
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3939
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Match
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716
700
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Database :

Result

Pred. No Score: Percent & Best Loc Query Ma DB:	: 8.59e-48 Length: 1210 716.00 Matches: 216 Similarity: 44.81% Conservative: 138 al Similarity: 27.34% Mismatches: 304 cch: 18.18% Indels: 30 7 Gaps: 30	
US-10-782	-570-1 (1-2235) x US-11-058-727-4 (1-1210)	
강 셤	1 GTGAATCAAAATAATAATAATGAATATGGATTATCGAAGAATTTATCTTATCCT 60 1:::::	
È	TTACACAATAATCCAAATCAACCATTA	
đ	1 SerAsnAspSerAsnArgfyrProPheAlaAsnGluProThrAsnAlaLeu 37	
රි සි	121 CAAAACACAAATTACAAAGAGTGGCTCAATATGTGTCAAGGGAATACACAATATGGT 177	
È	8 GATAATTTCGACACATTTGCTGGTGCTGATTGCTGCAGTTAGTGCAGGTACTATT 237	
đ	58 GlySerProGluValLeuValSerGlyGlnAspAlaAlaLysAlaAlaIleAsp 75	
දු දු	238 GTATCCGGTACCTGTTAGCCGGTATAGGTGGGCTCACTTCTATATCCGGACCGATAGGA 297 :::	
È	TACCCTAATCACTGTCTTTTGGCCCGGGGA 357	
q	107	
ò	CAAGAC	
qq	108 GlnLysSerGlnTrpGluIlePheMetGluGInValGluGluLeuIleAsnGln 125	
Ġ :	CCGTTAACAGAAAGCATAAAACAGCTAAAAGTTACAAACTTTAGAAGATTTAGACAAATA 477	
Q	LysileAlaGluTyrAlaArgAsnLysAlaLeuSerGluLeuGluGlyLeuGlyAsnAsn 14	
è 1	TTACAAAGCTATAATACAGCATTAGATGAGAAAAATTAAAAAGACTACAAGCTCCT 537	
8 8	146 IYIGIILLEUINYELEUINEALALEUGIUITPHYBGIU	
; a	AsnProAsnGlySerArgAlaLeuArgAspValArgAsnArgPheGlu 174	
Š ·	B AATGITCACAATGATTITTATTCGAGAAATACCTGGTTTCCAACTTGAAACTTATAAAACG 6	
අ	75 IleLeuAspSerLeuPheThrGlnTyrMetProSerPheArgValThrAsnPheGluVal 19	
충 움	658 CINTIACTROTRITANGGCAAGCTGCTAATTTTCATTTAAATTTATTACAACAAGGT 717 195 PropheleuthrValtyxThrGlinlaAlaAahaLeutheuteuteuteuteuteuteuteuteuteuteuteuteute	
È	ATGCT 777	
a	115 SerilePheGlyGluTrpGlyTrpSerThr 225	
8 8	GGAACATCAGATGACTATTATAAACTTTTAAAAGAAAATATACCTAAATATAGTAACTAT 83	
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දි දි	838 TGTGCAAATACCTATAGAGACTAAATAAACTTCGAAACGAACCTAATATGAGATGG 897	
È	TATCGCTCAA 957	
ą	266 ValAspTyrAsnGlnPhcArgArgGluMetThrLeuThrValLeuAspValValAlaLeu 285	
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TTTTCTTTTTATGATATAAGAGATACAAAGATTCAATAGGAAGAATAGGTGGCATTAAA 1017
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           178 GATAATTTCGAGACATTTGCTAGTGCTGATACAATTGCTGCAGTTAGTGCAGGTACTATT 237
                                                                                                                         238 GTAICCGGTACTCTGTTAGCCGGTATAGGTGGGCTCACTTCTATATCCGGACCGATAGGA 297
                                                                                                                                                                                                           :::||| |||:::|||
PheValGlyProlleValSerLeuTyrThrGlnLeuIleAspIleLeuTrpProSerGly 107
                                                                                                                                                                                                                                                    GAACAAGACAAAACAGTATGGACACAATTTAAAAATGGGAGAAATTTTTGTTGATACA 417
                                                                                                                                                                                                                                                                   418 CCGTTAACAGAAAGCATAAAACAGCTAAAGTTACAAACTTTAGAAGGATTTAGACAAATA 477
                                                                                                                                                                                                                                                                                                                                          598 AAIGITCACAAIGAITITIAITCGAGAAAIACCIGGITITCCAACIIGAAACITAIAAAACG 657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTATTACTACCTATTTATGCGCAAGCTGCTAATTTTCATTTAAATTTTACAACAAGGT 717
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CAAAACACAAATTACAAAGAGTGGCTCAATATGTGTCAAGGGAAT---ACACAATATGGT 177
                                                                                  ||||||| :::|||||||:::::||| ||| ||| :::::||| 38 GlnAsnMetAspTyrLysAspTyrLeuLysMetSerAlaGlyAsnAlaSerGluTyrPro
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76 IleValGlyLysLeuLeuSerGlyLeuGly-------
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SerIlePheGlyGluGluTrpGlyTrp------
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|LeuGluAlaAlaLysAlaValAsnAlaLeuPheThrAsn---ThrLysAspGlyLeu 694
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                                                                -------Pro
                                                                                                                      PhelleThrLeuGlyAlailePheGluAlaGluAspPheLeuGlyIleGluAlaTyrile
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JAPPLICANT: ADDAG
APPLICANT: Ronald D. Flannagan
APPLICANT: Renald D. Flannagan
APPLICANT: Refael Hermann
APPLICANT: Theodore W. Kahn
APPLICANT: Balbert L. Lu
APPLICANT: James K. Presnail
APPLICANT: James K. Presnail
APPLICANT: Gao-Guo Yu
TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
TITLE OF INVENTION: Ganes Encoding
FILE REFERENCE: 35718/291049
CURRENT FILING DATE: 2002-04-18
PRIOR APPLICATION NUMBER: 60/460,787
PRIOR APPLICATION NUMBER: 60/460,787
PRIOR PILING DATE: 2003-04-04
PRIOR FILING DATE: 2003-04-04
PRIOR FILING DATE: 2003-06-25
NUMBER OF SEQ ID NOS: 134
SOFTWARE: FastSEQ for Windows Version 4.0
TENENTH: 1.10
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216
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Mismatches:
Indels:
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Matcheg:
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Publication No. US20050261188A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : Bacillus thuringiensis
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716.00
44.81%
27.34%
18.18%
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US-11-108-389-4
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                                     2203 AATATAGAAGCCACAAACTATGATATTGAT 2232
                                                    ; Sequence 4, Application US/11192801; Publication No. US20050273882A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                              ORGANISM: Bacillus thuringiensis
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US-11-192-801-4
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------TACGGGAATCGTTTAGTTGGTATTGCGAATCGTAATAGATCTTAT 1230
                                                                                                1291 TTAATACCATTTGAATCCTATAAGTT----TCAATTGTAACTGATAGACAAGTAACTCCT 1347
                                                                                                                                                                                                  TTAAATAATTCACCTAGTAATAAATTAACATATTCAGCTGGGGGAATTTATCTAATGAT 1458
                                                                                                                                                                                                                                                                                                                                                      TATAGTCATATTTTATCCCAGTTTTCTTTTAATTATTACTATAAAATTGGATTAGCG 1602
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                                                                                                               ||| :::||| :::||| ::-
---PheAspPheThrAsnIyrAspIleTyrLysThrLeuSerLysAspAlaValLeuLeu 417
                                                                                                                                                                                                                          MetValAsn-----GlnLeuAsnAsnThr 445
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TyrserhiakrgleucyshialleThr------
                                                                ||||||| ::: ::::::||| ::: AgpileValPheProGluYatThrTyrIlePhePheGluWelGluValGluPhePhe
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                                                GCTACGACAGGAACTGAAATTATATATGGAGAAAGAACAGGTCCACCACAAAAAACT
                                                                                                                                                 ACTICCCCTITITCCIAAC-----AIAIACTITACAATIAAATCAAATIGAACTITAT
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                                                                                                                                                                                                                                                                                                      -----AATCCAAATTGTTTACCAAGCTATAATAGT
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APPLICANT: Romano, Charles P.

TITLE OF INVENTION: Improved Expression of Cry3Bb Insecticidal Protein in Plants FILE REFERENCE: 38-21(15304) Cry3Bb Improved Exp. Corn
CURRENT APPLICATION NUMBER: US/11/192,801
CURRENT FILING DATE: 2005-07-29
PRIOR APPLICATION NUMBER: US/10/232,665
PRIOR APPLICATION NUMBER: US/09/377,466
PRIOR PILING DATE: 1999-08-19
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 4
231
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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1816 AATTCTACACAATCTTATTACATTAGACTTCGATACGCTACAAATGGTGCTGGAAATACT 1875
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541 LeuPheLeuLysGluSerSerAsnSerIleAlaLysPheLysValThrLeuAsnSerAla 560
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Sequence 2, Application US/11058727

Publication No. US2005026148341

SEGNERAL INFORMATION:
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APPLICANT: Rafael Hermann
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APPLICANT: Albert L. Lu
APPLICANT: Albert L. Lu
APPLICANT: Albert L. Lu
APPLICANT: Gao-Guo Yu
APPLICANT: Gao-Guo Yu
APPLICANT: James F.H. Wong
APPLICANT: Gao-Guo Yu
APPLICANT: Gao-Guo Yu
APPLICANT: Cao-Guo Yu
FILES OF INVENTION: Genes Encoding Proteins With Pesticidal
TITLE OF INVENTION: Genes Encoding
FILES REFERENCE: 35718/287809
CURRENT APPLICATION NUMBER: 60/391,786
PRIOR APPLICATION NUMBER: 60/460,787
PRIOR PILING DATE: 2003-04-04
PRIOR PILING DATE: 2003-04-04
PRIOR PILING DATE: 2003-04-04
PRIOR PILING DATE: 2003-04-04
PRIOR PILING DATE: 2003-06-25
NUMBER OF SEQ ID NOS: 134
SEQ ID NO 2
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-----ThrProLeuSerLeuArgSerLysArgSerGlnAspArgIleArgGluLeu 170
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242 AspHisCysValAsnTrpTyrAsnValGlyLeuAsnGlyLeuArgGlySerThrTyrAsp 261
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126 LysileAlaGluTyrAlaArgAsnLysAlaLeuSerGluLeuGluGlyLeuGlyAsnAsn 145
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215 SerllePheGlyGluGluTrpGlyTrp-------SerThr 225
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138
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                                                                  Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                               US-10-782-570-1 (1-2235) x US-11-058-727-2 (1-1206)
; LENGTH: 1206
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-11-058-727-2
                                                                1.72e-46
699.00
45.26$
27.43$
17.75$
                                                                                     Percent Similarity:
Best Local Similarity:
Query Match:
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                                                       Alignment Scores
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1126 GGGCTTAGATTATTTTCATTTTTAGATGAACTTATATTTTTATACAAAAAATGAAACGTAC 1185
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246 CysValLysTrpTyrGluThrGlyLeuAlaLysLeuLysGlyThrSerAlaLysGlnTrp 265
                                        266 VallapityrdanglnPheArgArgGluMetThrLeuAlaValLeuAspValValAlaLeu 285
                                                                                                  ||| ::: ||| || 286 PheProAsnTyrAsBThrArgThrTyrProMetGlu-------ThrLys 299
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                                                                                  TITICITITIATGATATAAAGAGATACAAAGATTCAATAGGAAGAATAGGTGGCATTAAA
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                                                                                               1972 TACGGAGATTTTGGGTATTTCCAATTTCCAAGTACAGTAACATTACCTTTAAATCGAAAC 2031
GCTACAAATGGTGGTGGAAATACTCTTCCTAATATATCTCTTACAATACCAGGAGTAATA 1911
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600 IleGlnMetProLygThrMetAsnProGly--------GluAspLeuThr 613
                                                                                                              SerLysThrPheLysValAlaAspAlaIleThrThrLeuAsnLeuAlaThrAspSerSer 633
                                                                                                                                                              586 AlaThraspAla---------AspilevalLeuHisValAsnAspAlaGln
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APPLICANT: Ronald D. Flannagan
APPLICANT: Ronald D. Flannagan
APPLICANT: Thecdore W. Kahn
APPLICANT: Thecdore W. Kahn
APPLICANT: Albert L. Lu
APPLICANT: James K. Presnail
APPLICANT: James K. Presnail
APPLICANT: Gao-Guo Yu
APPLICANT: Cao-Guo Yu
APPLICANT: Cao-Guo Yu
TITLE OF INVENTION: Genes Bncoding Proteins With Pesticidal
TITLE OF INVENTION: Genes Bncoding Proteins With Pesticidal
TITLE OF INVENTION: Genes Bncoding Proteins With Pesticidal
FILE REFERENCE: 35718/291049
CURRENT APPLICATION NUMBER: U6/11/108,389
CURRENT FILING DATE: 2005-04-18
PRIOR APPLICATION NUMBER: 60/460,787
PRIOR APPLICATION NUMBER: 60/460,787
PRIOR APPLICATION NUMBER: 10/606,320
PRIOR FILING DATE: 2003-04-04
PRIOR FILING DATE: 2003-06-25
NUMBER OF SEQ'ID NOS: 134
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Bacillus thuringiensis
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---ACTIACCTIGAAATICAACCCAAICTCGCIAIAAIGGAAIAIAITIAACACGITCA 1125
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                                                                                                                                                                                                                  178 GATAATITCGAGACATTTGCTAGTGCTGATACAATTGCTGCAGTTAGTGCAGGTACTATT 237
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286 PheProAsnTyrAspThrAxgThrTyrProMetGlu-------ThrLys
                                                                                                                                                                                                                                                   GlySerProGluValLeuValSerGlyGlnAsp-----AlaAlaLysAlaAlaIleAsp
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                                                           TCTAACAGAAATATTGATCATTCTAGATACCCTTACACAAATAATCCAAAATAACCCATTA
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1126 GGGCTTAGATTATTTTTTAGATGAACTTATATTTTTACAAAAATGAAACGTAC 1185
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                                                    359 SerSerAlaArgTyrIleArgHisTrpAlaGlyHisGlnIleSerTyrHisArgValSer 378
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GlySerTrpTyrAspLysAlaProSerPheGlyValIleGluSerSerValIleArgPro 339
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446 Argly8ThrLeuLy8TyrAsn---ProValSerLy8AspIleIleAlaSerThrArgAsp 464
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600 IleGlnMetProLygThrMetAsnProGly--------GluAspLeuThr 613
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OTHER INFORMATION: Description of Artificial Sequence: synthetic or OTHER INFORMATION: non-naturally occurring amino acid sequence encoded by SEQ ID NO:
                                                                                                                                                                                                                                                                                                          Insecticidal Protein in Plants
Corn
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2080 ATTGATAAATTTGAATTTATACCAATTACTTCCTCTGTACGCCAAAATAGAGAAAAACAA 2139
                61 TCTAACAGAAATATTGATCATTCTAGATACCCTTACACAAATAATCCAAATCAACCATTA 120
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58 AspAsn-----SerThrValLysAspAlaValGlyThrGlyIle 70
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                                                                  ||| serGluLeuGlnThrAsnHiBAsnGlnTyrProLeuAlaAspAsnProAsnSerThrLeu
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| Sequence 6, Application US/11192801
| Publication No. US20050273882A1
| Publication No. US20050273882A1
| GENERAL INFORMATION: Improved Expression of Cry3Bb Inset TILLE OF INVENTION: Improved Expression of Cry3Bb Inset FILE REFERENCE: 38-21 (15304) Cry3Bb Improved Exp. CURRENT APPLICATION NUMBER: US/11/192,801
| CURRENT APPLICATION NUMBER: US/01-29
| PRIOR FILING DATE: 2005-08-29
| PRIOR FILING DATE: 1999-08-19
| NUMBER OF SEQ ID NOS: 43
| SOFTWARE: Patentin Ver. 2.0
| SEQ ID NO 6: SEQ ID NOS: 43
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Matches:
Conservative:
Mismatches:
Indels:
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|LeuArgProGlyValThrAspTyrGluValAsn 700
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US-11-192-801-6
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243 HisCysValAsnTrpTyrAsnValGlyLeuAsnGlyEeuArgGlySerThrTyrAspAla 262
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334 LeuPheAspTyrLeuGlnGlyIleGluPheHiBThrArgLeuGlnProGlyTyrPheGly 353
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ProPheAlaGlyAlaLeuThrSerPheTyrGlnSerPheLeuAsnThrIleTrpProSer 102
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APPLICANT: Romano, Charles P.

TILLE OF INVENTION: Improved Expression of Cry3Bb Insecticidal Protein in Plants FILLE REFERENCE: 38-21(15)34) CTY3Bb Improved Exp. Corn
CURRENT APPLICATION NUMBER: US/11/192,801
CURRENT FILING DATE: 2005-07-29
PRIOR APPLICATION NUMBER: US/10/232,665
PRIOR PILING DATE: 2002-08-29
PRIOR FILING DATE: 1999-08-19
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2.
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   ---ACATATTCAGCT--- 1437
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569 ArglleArgTyrAlaSerThr-------ThrAsnLeuArgLeuPheVal 582
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635 ValSerAsnGluLys11eTyrIleAspLys11eGluPheileProVal 650
1390 GAACTTTTAAATAATTCACCTAGTAATAAATTA----
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US-11-192-801-2
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TYPE: PRT ORGANISM: Bacillus thuringiensis

LENGTH: 652

US-11-192	-192-801-2						
Alignment S	cores:					අු	263 TrpVall
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qq	::: 38 GluGluLeuAsnTy	::: rrLysGluPhe	 LeuArgMetThrGl	:::	Leu 57	අු	
ò	178 GATAATTTCGAGAC	ATTTGCTAGE	GCTGATACAATTGC	GATAATTTCGAGACATTTGCTAGTGCTGATACAATTGCTGCAGTTAGTGCAGGTACT	ACT 234	ò	1222 TCTACTI
· A			::: SerThrValLy	SerThrValLysAspAlaValGlyThrGlyIle		Ωρ	371 IleGlyS
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8		TGATTTATT	CGAGAATACCTGG	GAGAATGTTCACAATGATTTTATTCGAGAATACCTGGTTTCCGAGCTTAAAA		È	1612 TTATATA
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ò	655 ACGCTATTACTACC	TATTTATGCG	CAAGCTGCTAATTT	TCATTTAAATTTACAA	CAA 714	È	
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1942 LysapSerPhekämiTyTTpSerdijämiTyTValGluThrkigFroSer 370 1222 TCTACTTATGCTACGACAGGAACTGAAATTATATATGAGAAACAGGTCCACCCAC
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988 GATTCAATAGGAAGAATAGGTGGCATTAAAACTGAACTTACAAGAGAAATTTATACAACT 1047
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162 IleThrArgleuAspGlyLeuGlyAsnValLeuAlaLeuTyrGlnLysAlaPheGluGlu 181
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APPLICANT: TANAKA, MAGGO
APPLICANT: YOKOYAMA, TOMOKO
APPLICANT: AOYAGT, MOTICAI
APPLICANT: AOYAGT, MACLO
APPLICANT: HASEGAWA, MAKOTO
APPLICANT: HASEGAWA, MAKOTO
APPLICANT: KIMURA, MAGABARU
APPLICANT: KIMURA, MAGABARU
APPLICANT: KIMURA, MAGABARU
APPLICANT: KIMURA, MAGABARU
APPLICANT: NISHIHASHI, Hideji
TITLB OF INVENTION: POLypepide having larvae growth inhibiting or
TITLB OF INVENTION: popuclectide encoding the same
TITLB OF INVENTION: popuclectide encoding the same
FILE REFERENCE: OP1335
CURRENT FILING DATE: 2005-03-29
FRIOR PILING DATE: 2001-04-13
FRIOR PILING DATE: 2001-04-13
FRIOR PILING DATE: 2001-07-04
NUMBER OF SEQ ID NOS: 22
SOFTWARE PATENTING DATE: 2001-07-04
SEQ ID NO 6

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Publication No. US20050246789A1
GENERAL INFORMATION:
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Sequence 8, Application US/11192801; Publication No. US20050273882A1; GENERAL INFORMATION:

RESULT 9 US-11-192-801-8

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by SEQ ID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64 AACAGAAATATTGATCATTCTAGATACCCTTACACAAATAATCCAAATCAACCATTACAA 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 AATTTCGAGACATTTGCTAGTGCTGATACAATTGCT---GCAGTTAGTGCAGGTACTATT 237
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APPLICANT: Romano, Charles P.

TITLE OF INVENTION: Improved Expression of Cry3Bb Insecticidal Protein in FILE REFERENCE: 39-21(15)304) Cry3Bb Improved Exp. Corn CURRENT APPLICATION NUMBER: US/11/192,801
CURRENT APPLICATION NUMBER: US/11/232,665
PRIOR APPLICATION NUMBER: US/09/377,466
PRIOR FILING DATE: 2002-08-29
PRIOR FILING DATE: 1999-08-19
SROFTWARE: PATENTING DATE: 1999-08-19
SNOFTWARE: PATENTING OF SEQ. ID NOS: 43
SOFTWARE: PATENTIN VET. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GluLeuGlnThrAsnHisAsnGlnTyrProLeuAlaAspAsnProAsnSerThrLeuGlu 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ||| |||||| :::|||::::|| ||| || AsnProAsnArgSerGluHisAspThrIle------LysValThrProAsnSer 19
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                                                                                                                                                                                                                                                                                                                                                                               sequence for Cry3Bb variant v11231 encoded
                                                                                                                                                                                                                                                                   FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: non-naturally
OTHER INFORMATION: occurring amino acid sequence encoded by SEQ ID NO:7
FEATURE:
NAME/KEY: PRT
LOCATION: (1) ..(653)
OTHER INFORMATION: amino acid sequence for Cry3Bb variant v11231 encoded
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207
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Matches:
Conservative:
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|ValValGlyGlnIleLeuGlyValValGly-----
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44.58%
28.05%
17.34%
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Query Match:
DB:
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US-11-192-801-8
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|ProValGlnLys-----LeuSerPheAspGlyGlnLysValTyr-----Arg 403
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                         ::: ||| ::: ::: ||| GlnAlaGluSerHisPheArgAsnSerMetProSerPheAlaValSerLysPheGluVal 193
                                                                                         CTATTACTACCTATTTATGCGCAAGCTGCTAATTTTCATTTAAATTTTACAACAAGGT 717
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Sequence 10, Application US/11192801

| Sequence 10, Application US/11192801
| Sequence 10, Application No. US20050273882A1
| Sequence 10, Application No. US20050273882A1
| GENERAL INFORMATION:
| APPLICANT: Romano, Charles P. |
| TITLE OF INVENTION: Improved Expression of Cry3Bb Insecticidal Protein in Plants |
| PILE REFERENCE: 38-21(1534) Cry3Bb Improved Exp. Corn |
| CURRENT APPLICATION NUMBER: US/11/192,801 |
| PRIOR PILING DATE: 2002-00-29 |
| PRIOR PILING DATE: 2002-06-29 |
| PRIOR PILING DATE: 1999-08-19 |
| NUMBER OF SEQ ID NOS: 43 |
| SEQ ID NO IN OS: 43 |
| SEQ ID NO IN OS: 43 |
| LENGTH: 653
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                                                                                         1725 ATATCAGATAAATAATTACAATGATCCCAGCAATCAAAGGTAACAGTCTTGATACAAAC 1725
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1606 AATATTATATACAGGTGCATTAGGATGGACACACAGTAGTAGTAATAGAAATAATGCA 1665
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PERATURE
OTHER INFORMATION: Description of Artificial Sequence: non-naturally
OTHER INFORMATION: occurring amino acid sequence encoded by SEQ ID NO:9
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                               ---ProPhePheThr------TrpThrHisArgSerValAspPhePheAsnThr
                                                                                                                                                                                    2053 GCAGATGTATCAAATTCAATTTAATCATTGATAAAATTGAATTTATACCAATT 2106
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LOCATION: (1)..(653)
OTHER INFORMATION: amino acid sequence encoded by SEQ ID
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US-11-192-801-10
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US-10-782-570	US-10-782-570-1 (1-2235) x US-11-192-801-10 (1-653)	è	1069 ACTURACY
Ş	4 AATCAAAATAATAATAATGAATATGAGATTATCGATTCAAAGAATTTATCTTATCCTTCT 63	ŝ	
Dp 3		Q	315 ThrLeu
9	AACAGAAATATTGATCGTTCTTAGATACCCTTTACAGAAATAATCCAAATCAACCATTAGA 123	È	1129 CTTAGA
	20 GluLeuGlnThrAsnHisAsnHisAsnGlnTvrProleuAlaAsnAsnBroAsnSerThrienGlu 39	a	334Hi8
-		È	1174
	40 GluLeuAshTyrLv8GluPheLeuArdMetThrGluAsoSerSerThrGluValLeuAso 59	q _Q	353 PheGly
		ò	1216 AATAGA
	01 ANIIILOONAN ANIINOCINGI GALACANI GCICCAGI INGI GCAGI ANII 237	qq	370 ProSer
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		ò	1336 CAAGTA
	PheAlaGlyAlaLeuThrSerPheTyrGlnSerPheLeuAsnThrIleTrpProSer	ପ୍ପ	404 Thrile
358		à	1384 CAAATT
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	CCGTTAACAGAAAGCATAAAACAGCTAAAAGTTACAAACTTTAGAAGGATTTAGAACAAATA	È	1435 GCT
		q	444 SerLys
		È	1486 GTAAAA
		q	462 ProGlu
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		È	1726 TCTAAG
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1069 A 315 T 1129 C 334 -		1336 C 404 T 1384 C 424 L 1435 G 444 S	1486 G 462 P 1546 A 474 S	1606 A 493 - 1666 A 508 I		568 A 1894 A 1954 A 1954 A 1954 A 1993 C

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-------AATGAAACGTACGGAATCGTTTAGTTGGTATTGCGAATCGT 1215
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              353 PheGlyLysAspSerPheAsnTyrTrpSerGlyAsnTyr-----ValGluThrArg 369
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                                                                                                                          ---ThrProLeuSerLeuArgSerLysArgSerGlnAspArgIleArgGluLeuPheSer 173
                                                                                                                                                                            CTATTACTACCTATTTATGCGCAAGCTGCTAATTTTCATTTAAATTTAATTTACAACAAGGT 717
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LyslleGluGluTyrAlaLysSerLysAlaLeuAlaGluLeuGlnGlyLeuGlnAsnAsn 141
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                                                                                             538 GGATTACCACCATCACCATTACAACAAGCTGCCTTGACTCTTAAAATACGATTTGAG
                                478 TTACAAAGCTATAATACAGCATTAGATGATTGGAGAAAATTAAAAAAGACTACAAGCTCCT
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TILLE OF INVENTION: Improved Expression of Cry3Bb Insecticidal Protein in Plants FILLE REPRENCE: 38-21(15334) Cry3Bb Improved Exp. Corn
CURRENT APPLICATION NUMBER: US/11/192, 801
CURRENT FILING DATE: 2005-07-29
PRIOR APPLICATION NUMBER: US/10/232, 665
PRIOR PILING DATE: 2002-08-29
PRIOR PILING DATE: 1999-08-19
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin Ver: 2.0
SEQ ID NO 12
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PheAlaGlyAlaLeuThrSerPheTyrGlnSerPheLeuAsnThrIleTrpProSer--- 103
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NAME/KEY: PRT
LOCATION: (1)..(1653)
OTHER INFORMATION: amino acid sequence encoded by SEQ ID NO:11
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; Sequence 12, Application US/11192801
; Publication No. US20050273882A1
; GENERAL INFORMÁTION:
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ORGANISM: Artificial Sequence
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---SerSerGluAspValAlaGluPheTyrArgArgGlnLeuLysLeuThrGlnGlnTyr
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                  Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                  2.63e-45
683.00
44.58%
28.05%
17.34%
                                                                    Percent Similarity:
Best Local Similarity:
Query Match:
DB:
Alignment Scores:
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OTHER INFORMATION: Description of Artificial Sequence: peptide encoded by SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 14, Application US/11192801
| Publication No. US20050273882A1
| Publication No. US20050273882A1
| GENERAL INFORMATION:
| APPLICANT: Romano, Charles P.
| TITLE OF INVENTION: Improved Expression of Cry3Bb Insecticidal Protein in Plants
| FILE REFERENCE: 38-21(15304) Cry3Bb Improved Exp. Corn
| CURRENT APPLICATION NUMBER: US/11/192,801
| CURRENT PILING DATE: 2005-07-29
| PRIOR PILING DATE: 2005-07-29
| PRIOR PILING DATE: 1999-08-19
| PRIOR FILING DATE: 1999-08-19
| NUMBER OF SEQ ID NOS: 43
| SEQ ID NO 14
| LENGTH: 653
                       GTAAAAAAAGACTGTAAACCAATTATTAATCCAAATTGTTTACCAAGCTATAATAGTTAT 1545
                                                                                                                                                                                                                                                                                                                               ATATCAGATAAAATAATTACAATGATCCCAGCAATCAAAGGTAACAGTCTTGATACAAAC 1725
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                                                                                                                                                                                                                          1606 AATATATATATACAGGTGCATTAGGATGGACACACAGTAGTGTTAATAGAAATAATGCA 1665
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        594 TyrileAsnLysThrMetAsnLysAspAspAspLeuThrTyrGlnThrPheAspLeuAla 613
                                                                         -----GluLysAlaTyr 473
                                                                                                                                                                           474 SerHisGlnLeuAsnTyrAlaGluCysPheLeuMetGlnAspArgArgGlyThrIle--- 492
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---ProPhePheThr------TrpThrHi8ArgSerValAspPhePheAsnThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGTCATATTTTATCCCAGTTTTCTTTATTTAATTATTCCTATAAAATTGGATTAGCGCTA
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634 SerPheValSerAbnGluLy91leTyrIleAbpLy8IleGluPheIleProVal 651
                                                  ProGluThrThrAspGluProLeu------
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NAME/KEX: PRT
LOCATION: (1). (653)
OTHER INFORMATION: Cry3Bb1 variant v11231
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US-11-192-801-14
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6 8 6 8 6 8 6 8 6 8 6 8 6 8 6 8 6 8 6 8	ATCGCTCAATTTTCTTTTATGATATAAAGAGATACAAAGAATAGAAGAAGAATAGGT	OY 1954 AATTATA Db 594 TYILLEA OY 1993 CAATTTC Db 614 ThrThrA OY 2053 GCAGATG CO 2054 SEFPEN CO 2054 SEFPEN CO 2055 GCAGATG CO 2056 GCAGTA CO 2056 GCACATG CO 2056 GCAC
8 8 8 8 8 8	1384 CAMATTGAACTTTATTTAAATAATTAA	/ MAME/KRY: PRT / LOCATION: (1)(6 / OTHER INFORMATION US-11.192-801-16 Alignment Scores: Pred. No.: Score: Fercent Similarity: Best Local Similarity Ouery Match: DB:
868686	1546 AGTCATATTTATCCCAGTTTTCTTTATTTAATTATTCCTATAAATTGGATTAGCGCTA 1605	US-10-782-570-1 (1-22 OY
86868686	1726 TCTAAGGTAATTGAAGGACCTGGTCATACAGGAGAAACTTGGTTTATTTA	

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CCAAGTACAGTAACATTACCTTTAAATCGAAACATACCATTTATATTAATCGT 2052
AAT------AATTTACAATACGGAGATTTTGGGTATTTC 1992
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adlyAlaLeuThrSerPheTyrGlnSerPheLeuAsnThrIleTrpProSer--- 103
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               ||| ::: ||||
|AsnSerAsnWetGlyPheSerGlyAspLysAsnGluLeulleIleGlyAlaGlu 633
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|GlyGlnIleLeuGlyValValGly------ValPro
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                                                                                                     GTATCAAATTCAATTTTAATCATTGATAAAATTGAATTTATACCAATT 2106
                                                                                                                      653
207
122
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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N: Cry3Bb1 variant v11231
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683.00
44.58%
28.05%
17.34%
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In Ver. 2.0
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Db 424 LygValAspPheSerGl	1606. 493 1666 508 1726	Seras TACAT :: Argva ACAAT :: Pheva AATTA	Oy 1993 CAATTTCCAAGTACAGT	APPLICANT: Romano, Charles F TITLE OF INVENTION: Improved FILE REFERENCE: 38-21(15304); CURRENT FILING DATE: 2005-0; PRIOR PELLING DATE: 2005-0; PRIOR PELLING DATE: 1999-08-1; PRIOR PELLING DATE: 1999-08-1; NUMBER OF SEQ ID NOS: 43 SOTTWARE: Patentin Ver. 2.0 SEQ ID NO 19 LENGTH: 653 TYPE: PRT ORGANISM: Artificial Sequer: FEATURE: NAME/KEY: PRT
	AATGTTCACAATGATTTTATTCGAGAAATACCTGGTTTCCAACTTGAAACTTATAAAACG :::	778 GGAACATCAGATGACTATTATAAACTTTTAAAAGAAAATATACCTAAATAT 828 ::: :: :: ::: :: :::	GGCATTAAAACTGAACTTACAAGAAATTATATAACTGAATTATGACGGTCTT	
8 8 8 8 8 8	8 6 8 6 8 6 8	6 8 6 8 6 8 6	8686868	888888888888888888888888888888888888888

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i P. ed Expression of Cry3Bb Insecticidal Protein in Plants (ed Expression of Cry3Bb Improved Exp. Corn it US/11/192,801 5:-07-29 US/10/232,665
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                                                                                             SGGAATTTATCTAATGATAAAAAAACAACTGATTTTCAATTTCCT 1485
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3luProLeu------GluLysAlaTyr 473
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iyaPheLygValThrLeuAsnSerAlaAlaLeuLeuGlnArgTyr 567
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                                                                           49 AICGCTCAAITITTCTITITATGATATAAAGAGATACAAAGATTCAATAGGAAGAATAGGT 1008
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                      29 CITAGATTATTTTCATTTTTAGATGAACTTATATTTTTTATACAAAA-----
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  PheAlaGlyAlaLeuThrSerPheTyrGlnSerPheLeuAsnThrIleTrpProSer ---
                              GAACAAGACAAAACAGTATGGACACAATTTTATTAAAATGGGAGAAATTTTTGTTGATACA
                                                       -----AspAlaAspProTrpLysAlaPheMetAlaGlnValGluValLeuIleAspLys
                                                                                                                                            TTACAAAGCTATAATACAGCATTAGATGATTGGAGAAAATTAAAAAGACTACAAGCTCCT
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TITLE OF INVENTION: Improved Expression of Cry3Bb Insecticidal Protein in Plants FILE REFERENCE: 38-21(15304) Cry3Bb Improved Exp. Corn CURRENT APPLICATION NUMBER: US/11/192,801
CURRENT APPLICATION NUMBER: US/10/23,665
PRIOR PILING DATE: 2005-07-29
PRIOR PILING DATE: 2005-07-29
PRIOR PILING DATE: 1999-08-19
NUMBER: OF SEQ ID NOS: 43
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 20
LENGTH: 653
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ThrThrAsnSerAsnMetGlyPheSerGlyAspLysAsnGluLeulleIleGlyAlaGlu 633
124 AACACAAATTACAAAGAGTGGCTCAATATGTGTCAA---GGGAATACACAATATGGTGAT 180
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AsnProAsnAsnArgSerGluHisAspThrIle-----'LysValThrProAsnSer 19
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; OTHER INFORMATION: Cry3Bb1 variant 11231mv1
US-11-192-801-20
                                         1954 AATTATAAT------
                                                                                                                                                                                                                                      Sequence 20, Application US/11192801; Publication No. US20050273882A1; GENERAL INFORMATION:
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à	1384	CAAATTGAACTTTATTTAAATAATTCACCTAGTAATAAATTAACATATTCA 1434
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à	1435	GCTGGGGGGAATTTATCTAATGATAAAAAACAACTGATTTTCAATTTCCT 1485
qq	444	SerLysArgAsnAsnGlyHisValSerAlaGlnAspSerIleAspGlnLeuPro 461
ờ	1486	1486 GTABAAAAAAGACTGTAAAACCAATTATTAATCCAAATTGTTTACCAAGCTATAATAGTTAT 1545
qq	462	FrogluthrThrAspGlubroLeu
ò	1546	
qq	474	SerHisGlnLeuAsnTyrAlaGluCysPheLeuMetGlnAspArgArgGlyThrIle 492
ò	1606	AATATTATATACAGGTGCATTAGGATGGACACACAGTAGTGTTAATAGAAATAATGCA 1665
qq	493	proPhePheThrTrpThrHisArgSerValAspPhePheAsnThr 507
à	1666	ATATCAGATAAAATAATTACAATGATCCCAGCAATCAAAGGTAACAGTCTTGATACAAAC 1725
QQ	508	
ò	1726	TCTAAGGTAATTGAAGGACCTGGTCATACAGGAGAAACTTGGTTTATTTA
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ò	1780	
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ò	1834	TACATTAGACTTCGATACGCTACAAATGGTGCTGGAAATACTCTTCCTAATATATCTCTT 1893
qq	268	
ò	1894	ACAATACCAGGAGTAATAGGAATACCACCTCAACGACTCAACAACAACAACTTTTTCTGGTACA 1953
qq	582	iii PheValGlnAsnSerAsnAsnAspPheLeuValIle 593
è	1954	1954 AATTATAATAATTTACAATACGGAGATTTTGGGTATTTC 1992
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qq	614	ThrThrAsnSerAsnMetGlyPheSerGlyAspLysAsnGluLeullelleGlyAlaGlu 633
à	2053	GCAGATGTATCAAATTCAAATTTTAATCATTGATAAAATTGAATTTATACCAATT 2106
a	634	ii:

Search completed: January 12, 2006, 06:43:15 Job time : 55 Bec8

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4, Appli 6, Appli 6, Appli 10, Appl 111, App 111, App 111, Appl 110, Appl 111, Appl 11

Perfect score:

Sequence:

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Scoring table:

Minimum DB Maximum DB

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Sequence 112, App
Sequence 110, App
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Sequence 98, A
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ZIP: 32606
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/224,024
                 US-08-996-441B-110

US-08-993-172A-110

US-08-993-170A-110

US-08-993-170A-110

US-08-973-170B-110

US-09-427-770-110

US-09-427-770-110

US-09-427-770-110

US-09-427-770-110

US-09-95-665-6

US-08-996-441B-14

US-08-996-441B-28

US-08-996-441B-28

US-08-996-441B-28

US-08-996-441B-111

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ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGIGTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: MA79
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-372-5800
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/856,226
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      Command line parameters:

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-MODEL=frame+ n.2b. model - DEV=xlp
-Q=/CGN22_1/USFTO Spool_D/USF10782570/runat_12012006_060222_7551/app_query.fasta_1.2375
-Q=/CGN22_1/USFTO Spool_D/USF10782570/runat_12012006_060222_7551/app_query.fasta_1.2375
-DB=1680ed_Patenfe AA - OFWAF=fastan - SUPFIX=xa1 - MINMATCH=0.1 - LOOPCGL=0
-LIST=E45 - DOCALIGN=200 - THR SOCRE=CAT - THR MAR-100 - THR MINDEN O. ALIGN=15
-MODES=LOCAL - OUTFWT=pto - NORM=ext - HEAPPSIZE=500 - MINLEN=0 - MAXLEN=200000000
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-NO_WARP - LARGEQUERY - NGG_CSORES=0 - WALT - DSPBLOCK=100 - LONGLOG
-DSV TIMEOUT=120 - WARN TIMEOUT=30 - THRRADES 1 - XGAPOP=10 - XGAPEXT=0.5 - FGAPOP=6
-FGAPEXT=7 - YGAPOP=10 - YGAPEXT=0.5 - DELOP=6 - DELOFET=7
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Copyright (c) 1993 - 2006 Compugen Ltd.
                                                                                      protein search, using frame_plus_n2p model
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US-08-315-468-4
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Maximum Match 100%
Listing first 45 summaries
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Matches:
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Mismatches:
Indels:
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INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 1180 amino acids
TYPE: amino acid
STRANDEDNESS: aingle
TOPOLLOGY: linear
MOLECULE TYPE: protein
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1153.00
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Percent Similarity:
Best Local Similarity:
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                                                         ACTITITICIGGIACAAATTATAATATTTACAATACGGAGATTTTGGGTATTTCCAATTT 1998
                                                                                                        1999 CCAAGTACAGTAACATTACCTTTAAATCGAAACATACCATTTATATTTAATCGTGCAGAT 2058
            1879 CCTAATATATCTCTTACAATACCAGGAGTAATAGGAATACCACCTCAACGACTCAACAAC 1938
                                                                                                                                                     ::: |||||||||:::|||| 641 SerAsnGluValLysPheAlaProAsnGlnAsnIleSerLeuValPheAsnArgSerAsp 660
                                                                                                                                                                                                                                                    TTCACAAATCATACAAAAAATACTTTAAATATAGAAGCCACAAACTATGATATTGAT 2232
                                                                                                                                                                                                                                                                 APPLICANT: Street address: 4980 Carroll Canyon Road
APPLICANT: City: San Diego
APPLICANT: State/Province: California
APPLICANT: State/Province: US
APPLICANT: Country: US
APPLICANT: Postal code/Zip: 92121
APPLICANT: Phone number: (619) 453-8030 Fax number:
APPLICANT: Telex number: TITLE OF INVENTION: Materials and Methods for the Control of TITLE OF INVENTION: Calliphoridae Pests
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/07902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: David R. Saliwanchik
STREBF: 2421 N.W. 418t Street, Suite A-1
CITY: Galnesville
STATE: FL
                                                                                                                                                                                                                                                                                                                          Sequence 28, Application PC/TUS9407902 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: SALINAMOLIAL, DAVID R.
REGISTRATION NUMBER: 31,794
REPERENCE/DOCKET NUMBER: MA79
TELECOMMUNICATION INFORMATION:
TELEPRAN: 904-375-8100
TELEPRAN: 904-372-5800
INFORMATION FOR SEQ ID NO: 28:
SEQUIBNIE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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TYPE: amino acid
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Alignment Scores:

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127 ACAAATTACAAAGAGTGGCTCAATATGTGTCAAGGGAATACACAATATGGTGATAATTTC 186
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112 AgnThr---TrpSerAgpPheIleThrGlnThrLygAgnIleIleLygLygGluIleAla 130
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282
131
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                    Matches:
Conservative:
Mismatches:
Indels:
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  Length:
  3.986-96
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54.41%
37.15%
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SerAsnGluVallysPheAlaProAsnGlnAsnIleSerLeuValPheAsnArgSerAsp 660
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                                                                                                                                                                                                                                                                 Sequence 31, Application US/09224024

Patent No. 605653

GENERAL INFORMATION:
APPLICANT: Leslie Hickle
APPLICANT: Jewel Payne
TITLE OF INVENTION: Materials and Methods for the Control
TITLE OF INVENTION: Calliphoridae Pests
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: David R. Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: FL
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/224,024
FILING DATE:
CLASSIFICATION:
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251
115
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Matches:
Conservative:
Mismatches:
Indels:
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NAME: Sallwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: MA79
TELECOMMUICATION INPORMATION:
TELEPHONE: 904-372-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/856,226
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
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TYPE: amino acid
MOLECULE TYPE: protein
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Best Local Similarity:
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 GATACTATCGCTCAATTTTCTTTTTTTTATAAAGAGATACAAAGATTCAATAGGAAGA 1002
                                                                                                                                                                                                                                                                                                                .234 ACGACAGGAACTGAAATTATATGGAGAAAGAACAGGTCCACCACCACAAAAACTTTA 1293
                                                                                                                                                                                                                                                                                                                                                                              1294 ATACCATTTGAATCCTATAAAGTTTCAATTGTAACTGATAGACAAGTAACTCCTACTTCC 1353
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1465 ACAACTGATTTTCAATTTCCTGTAAAAAAGACTGTAAACCAATTATTAATCCAAATTGT 1524
                                                                               -----GlyValGlnSerGluLeuThrArgGluIleTyrGlnVal---LeuAsnPheGlu 337
                                                                                                                                               ArgPro---HisLeuPheThrTrpLeuAspSerLeuAsnPheTyrGluLysAlaGlnThr 374
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ThrProAsnAsnPhePhe---ThrSerHisTyrAsnMetPheHisTyrThrLeuAspAsn 393
                                                                                                                                                                                                                                                                                                                                      602 AlaValIleAsnLeuSerIleProGlyValAlaGluLeu---GlyMetAlaLeuAsnFro 620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          432 LysTyrLeuAsnAspTyrAsnAsnIleSerLysMetAspPhePheIleThrAsnGlyThr 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               582 PheGlnGlnSerTyrPheIleArgIleArgTyrAlaSerAsnGlySerAlaAsnThrArg 601
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AgpieuValAlaLeuPheProAsnTyrAspValGlyLysTyrProlle-----
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                                                             .063 CGTCTTACTTACCTTGAAATTCAACCCAATCTCGCTATAATGGAATATAATTTAACACGT
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CAAAAC	льувавг гартто	AsnAla	ATCCGG1	valdiy	ATAGG	ValLeuAlaAlaGly	ACAAGAC	TTAAC	::: ollegh	ACAAAT2	: sAsnGlr	AGCTCCT		ATTTGAC	rLeuGlı	rgaaac: :	ProTh	TTATT	Teuler	AATTGA	yileAsı	ACCTAA	eGlnGl	CGAACC	rAsnTh	ATTAGA	LeuAsi	AAGAATI		TGACCG:	raspīhi		, , , , , , , , , , , , , , , , , , ,
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attgatcattctagatacccttacagaataatccaaatcaaccattacaaaacacaat	oAsnGl:		TTTGCTAGTGCTGATACAATTGCTGCAGTAGTACTATTGTATCCGGTACTCTG	PheValSerSerGluThrileValGlyValSerAlaGlyIleIleValValGlyThrMet	TTAGCCGGTATAGGTGGGCTCACTTCTATATCCGGACCCATAGGAATAATAGGTGCTATA	aPro	Analaictitiggracccnaraicactorititiggcccgcggaagaacaagacaaaaca 	GTATGGACACAATTTATTAAAATGGGAGAAATTTTTGTTGATACACGGTTAACAGAA	G1	-agcataaaacagctaaagttacaaactttagaaggatttagacaaatattacaa		AGCTATAATACAGCATTAGATGATTGAGAAAATTAAAAAGACTACAAGCTCCTGGATTA	aArg	CCACCATCATCAGCATTACAACAAGCTGCCTTGACTTTAAAATACGATTTGAGAATGTT ::: ::: :::	ThrHibAlaAsnAlaLysAlaValHisAspLeuPheThrThrLeuGluProIle	GATTTTATTCGAGAAATACCTGGTTTCCAACTTGAAACTTATAAA	IleAspLysAspLeuAspMetLeuLysAsnAsnAlaSerTyrArgIleProThr	acgetattactacctatttatgegeagetgetaatttteatttaattta	-LeuProAlaTyrAlaGlnIleAlaThrTrpHisLeuAsnLeuLeuLysHis	GGTGCTGAATTGGCTGATGGAATGCAGATATACATCCTTCACAAATTGAACCTAAT	LeuglnAsnGlnGlyileAsnProSer	GCTGGAACATCAGATGACTATTATAAACTTTTAAAAGAAAATATACCTAAATATAGT	::: ::: ThrPheAsnSerSerAsnTyrTyrGlnGlyTyrLeuLysArgLysIleGlnGluTyrThr	AACTATTGTGCAAATACCTATAGAGAAGGACTAAATAAACTTCGAAACGAACCTAATATG		AGATGGAGTATATTAAAGATAATGAAGATATATGACTATTACTGTATTAGATACTATC	ThrirpasnMetTyrasnThrTyrargLeuGluMetThrLeuThrValLeuAspLeuIle	GCTCAATTTTTTTTTTATGATATAAAGATACAAAGATTCAATAGGAAGAATAGGTGGC	AlailePheProAsnTyrAspProGluLysTyrProIle	ATTAAAACTGAACTTACAAGAGAAATTTATACAACTGAAATAAAT	Vally8SerGluLeuThrArgGluVallyrThrAsnvalAsnSerAspInrPheArg maxormmoaaammoaaaccocaammaaacaccaammaaacaccaammaacaccaammaacaccaammaacaccaammoacaccaammaacaccaammoacaccaammaaca		Torrawn.
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115 ValTrpGlnAspLeuLeuAsnIleGly------GlyArgProIleGlnGluIle 130
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                                                  TITGCTAGTGCTGATACAATTGCTGCAGTTAGTGCAGGTACTATTGTATCCGGTACTCTG 252
                                                                                                                                                 Leugly------ValLeuAlaAlaPheAlaAlaPro----ValLeuAlaAlaGly 95
 GTATGGACACAATTTAAAATGGGAGAAATTTTTGTTGATACACCGTTAACAGAA---
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                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Materials and Methods for the Control of TITLE OF INVENTION: Calliphoridae Pests
TOWNER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                               4980 Carroll Canyon Road
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/07902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                          SBE: David R. Saliwanchik
: 2421 N.W. 418t Street, Suite A-1
Gainesville
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Matches:
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                                                                                                                                                                                                                                                Country:

Bostal code/Zip: 92121

Phone number: (619) 453-8030

Telex number:
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                                                                                                                                              Sequence 31, Application PC/TUS9407902 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: SYMPHY PC COMPATIBLE
COMPUTER: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: SAI!WANCHIK, DAVIG R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: MA79
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEPHONE: 904-372-5800
                                                                                                                                                                                               Street address:
City: San Diego
State/Province:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 686 amino acids
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STRANDEDNESS: single
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STREET: 24
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                                                                                                       |||| ::: ::: ::: ::: ::: SefTyrlleLysThrAspAsnTyrllePheSerVal------ValArgGluArgArg 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      582 IleSerValGlu---LeuProSerThrThrSerArgGlnAsnProAsnAlaThrAspLeu 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     374 ---PheThrHisThrAsnAspAspArgAsnileIleTrpGlyAlaValHisGlyHisIle 392
                                                                                                                                                                         413 GluilevalArgHisArgGlu-------TyrSerAsp 422
                                                                                                                                                                                                                                423 IlelleTyrGluMetIlePhePheSerAsnSer---SerGluValPheArgTyrSerSer 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   636 SerTyrAsnile---TyrileAspLysileGluPheileProileThrGlnSerValLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                              489 ArgvalAlaPheSerTrpThrHisThrServalAspPheGlnAsnThr1leAspLeuAsp
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                             ---CCACCCACAACAAAACTTTTAATACCATTTGAATCCTAT-----AAAGTT
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360 AspProTyrAspIlePheSerPheThrGlyAsnGlnMetAla-
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APPLICANT: Michaels, Tracy Bllis
APPLICANT: Poncerrada, Luis
APPLICANT: Poncerrada, Luis
APPLICANT: Narva, Kenneth B.
TITLE OF INVENTION: Process for Controlling Scarab Pests
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSER: David R. Saliwanchik
STREET: 2421 N.W. 418t Street, Suite A-1
CITY: Gainesville
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216
152
297
109
28
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MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC COMPALIDLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version #1.25
GURRANT APPLICATION DATA:
APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LIBRARY: LambdaGEM-11 library of L. Foncerrada
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Mismatches:
Indels:
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Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/014,941
FILING DATE: 01 FEB 1993
APPLICATION NUMBER: 07/828,430
FILING DATE: 30-JAN-1992
PRIOR APPLICATION DATE:
APPLICATION NUMBER: 07/808,316
FILING DATE: 16-DEC-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REGISTRAPEROCOMPATION TREECOMMUNICATION INPORMATION:
TELEPHONE: 904-375-8100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Bacillus thuringiensis
; Sequence 4, Application US/08315468; Patent No. 5554534; GENERAL INFORMATION:
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SEQUENCE CHARACTERISTICS:
LENGTH: 1169 amino acids
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787.50
47.55%
27.91%
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INDIVIDUAL ISOLATE: 50C
IMMEDIATE SOURCE:
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MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: single
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US-10-782-570-1 (1-2235) x US-08-315-468-4 (1-1169)

1 GTGAAICAAAATAATAATAATGAATATGAGATTATGGATTCAAGGATTTATCCT 60

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8 6 8 6

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2010 -----TTATTTTCATTTTTAGATGAACTTATATTTTATACA 1170 1288 ACTITA----TCAATTGTAACCATTTGAATCCTATAAAGTT---TCAATTGTAACT 1329 --- 1368 -----TACTITACAATTAATCAAATTGAACTTTAATTAAATAAATTCACCTAGT 1416 1417 AATAAATTAACATATTCA---GCTGGGGGAATTTATCTAATGATAAAAAAACAACTGAT 1473 1474 TTTCAATTTCCTGTAAAAAGACTGTAAACCAATTATTAATCCAAATTGTTTACCAAGC 1533 1654 AGAAATAATGCAATATCAGATAAATAATTACAATGATCCCAGCAATCAAAGGTAACAGT 1713 TTACAAAGTCAA---GGGCGTTTAGAGATTACATGTAGAACTCCTAATTCTACACAATCT 1830 1891 CTTACAATACCAGGAGTAATAGGAATACCACCTCAACGACTCAACAACACTTTTTCTGGT 1950 2011 ACATTACCTTTAAATCGAAACATACCATTTATATTTAATCGTGCAGATGTATCAAATTCA 2070 2071 ATTTTAATCATTGATAAATTGAATTTATACCAATTACTTCCTCTGTACGCCAAAATAGA 2130 374 TyrLysHisIledlyThrSerSerThrPheThrGlnMetTyrGly-----ThrAsnGln 391 :::||| :::||| :::||| 432 ProGluThrGluPhePheMetValAsnGlnLeu------AsnAsnThrArg 446 467 LeuGluLeuProProGluThrSerGlyGln-----------------ProAsn 478 1594 GGATTAGCGCTAAATATATATATACAGGTGCATTAGGATGGACACACAGTAGTGTAAT 1653 512 513 LeuThrAsnThrValLysSerGlyGluIleThrGlnIleProGlyGlyLysSerSerThr 532 1714 CTTGATACAAACTCTAAGGTAATTGAAGGACCTGGTCATACAGGAGGAAACTTGGTTTAT 1773 571 606 LysAsnGluAsnAspLeuThrTyrAsnAspPheLysTyrIleGluTyrProArgVal1le 625 ServalAsnAlaSerSerAsnIleGlnArgLeuSerIleGlyIleGlnThrAsnThrAsn 645 392 AsnLeuGlnSerThrSerAsnPheAspPheThrAsnTyrAspIleTyrLysThrLeuSer 411 412 AsnGlyAlaValLeuLeuAspIleValTyrProGlyTyrThrTyrThrPhePheGlyMet 431 ----SerSerThrSerThrTyrValProValPheSerTrpThrHisArgSerAlaAsp AAAAATGAAACGTAC---GGGAATCGTTTAGTTGGTATTGCGAATCGTAATAGATCTACT ::: |||||||::|||||||||PheArgll 1951 ACAAATTATAATAATTACAATACGGAGATTTTGGGTATTTCCAATTTCCAAGTACAGTA 1330 GATAGACAAGTAACTCCCTACTTCCCTATTCCTAACATA-----CGTTCAGGGCTTAGA-1774 1111 1534 646 1228 1369 447 495

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nt Similarity: 44.27% Cons Local Similarity: 28.80% Mism Match: 17.92% Inde		1 GTGAATCAAAATAATAATGAATATGAGATTATGGATTCAAAGAATTTATCTTAT	en 20	CCTTCTAACAGAAATATTGATCATTCTAGATACCCTTACACAAATAATCCAAATCAACCA		OY 118 TTACAAAACACAAATTACAAAGAGTGGCTCAATATGTCAAGGGAATACACAATATGGT 177	Db 37 LeuGluGluLeuAsnTyrLysGluPheLeuArgMetThrAlaAspAsnSerThr 54	Qy 178 GAIAATTTCGAGACATTTGCTAGTGCTGATACAATTGCTGCAGTTAGTGCAGGTACTATT 237	Db 55GluvalLeuAspSerSerThrValLysAspAlaValGlyThrGlyIleSer 71	Qy 238 GTATCCGGTACTCTGTTAGCCGGTATAGGTCGGCTCACTTCTATATCCGGACCGATAGGA 297		298	::: ::: ::: :::	#U ### #U ############################	358 GAACAAAAAAAGIAIGGACACAAAIIIAIIAAAAIGGAAAAAAIIIIIGGAAAAAAIIIIGGAAAAAA	103AspAlaAspProTrpLysAlaPheMetAlaGinValGilvalLeulleAspLys	418 CCGTTAACAGAAAGCATAAAGCTTACAAACTTTAGAAAGAA	121	478 TIACAAAGCIATAATACAGCATTAGATGATTGAGAAAAATTAAAAAGCIACAT :::	141 PheGluAspTyrValAsnAlaLeuAspSerTrpLysLys	538 GGATTACCACCATCATCAGCATTACAAGAGCTGCCTTGACTCTTAAAATACGATTTGAG		598 AATGTTCACAATGATTTTATTCGAGAAATACCTGGTTTCCAACTTGAAACTTATAAAACG 6		658 CTATTACTACCTATTTATGCGCAAGCTGCTAATTTTTCATTTAAATTTTATTACAAGGT		Qy 718 GCTGAATTGGCTGATGGAATGCAGATATACATCCTTCACAAATTGAACCTAATGCT 777	Db 213 GlnValPheGlyGluTrpGlyTyr221	Qy 778 GGAACATCAGATGACTATTATAAACTTTTAAAAGAAATATACCTAAATAT 828	Db 222SerSerGluAspIleAlaGluPheTyrGlnArgGlnLeuLysLeuThrGlnGlnTyr 240		56	889 AIGAGAIGGAGTATATTAAIGATATATCGAAGATATATGACTATTACTGTATTAGATACT	Db 261 AspAlaTrpValLysPheAsgArgPheArgArgGluMetThrLeuThrValLeuAspLeu 280	Qy 949 AICGCICAAITITCITITIAIGAIAIRAAGAGAIACAAAGAITCAAIAGGAAGAAGAIAGGI 1008
Oy 2131 GAAAAACAAAAATTAGAAACTATCCAAACAAAAATAAATA		NT 6	US-08-315-468-6 ; Sequence 6, Application US/08315468	Patent No. 5554534 GENERAL INFORMATION:	APPLICANT: Michaels, Tracy Ellis	APPLICANT: FOLCETRUS, DATE APPLICANT: Narva, Canada B. Tritis OF INVENTION. Drocess for Controlling Scarsh Dests	TITLE OF INVENTION: FIGURES TOT CONCIOLING SCALED FEBGE TOTAL OF INVENTION: with Bacillus thuringionsis Isolates	CORRESPONDENCES: 6	; ADDRESSER: David R. Saliwanchik ; STREET: 2421 N.W. 41st Street, Suite A-1		; COUNTRY: USA ; ZIP: 32606	85 5	COMPUTER: IBM PC Compatible	SOPTWARE: Patentin Release #1.0, Version #1.25	; CURRENT APPLICATION DATA: ; APPLICATION NUMBER: US/08/315,468	; FILING DATE: ; CLASSIFICATION: 424		; FILING DATE: 01 FEB 1993 ; APPLICATION NUMBER: 07/828,430	; FILING DATE: 30-JAN-1992 ; PRIOR APPLICATION DATA:	APPLICATION NUMBER: 07/808,316 FILING DATE: 16-DEC-1991	; ATTORNBY/AGENT INFORMATION: ; NAME: Saliwanchik, David R.	REGISTRATION NUMBER: 31,794 REPRENCY/DOCKET NIMBER: MA73.C2	Ęs	; TELRFAX: 904-372-5800 ; INFORMATION FOR SEQ ID NO: 6:	; SEQUENCE CHARACTERISTICS: ; LENGTH: 651 amino acide	TYPE: amino acid	TOPOLOGY: 11near	/ MOLECULE TIES: PIOCETH // HYPOTHETICAL: YES	Е.	_	INDIVIDUAL ISOLATE: 43F ; IMMEDIATE SOURCE: : CTANE: R. CO'I XII-Rlue (DM1.98-4). NRRL B-18291	FEATURE: 1. COLL ALL LICO (FILE) CO. 1. MINERAL MANAGEMENT CO. 1. MANAGEMENT CO. 1. MANAGEMENT CO. 1. MINERAL MANAGEMENT C		National Despite	Alignment Scores: 1.37e-55 Length: 651 Pred. No.: 706.00 Matches: 216

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                      2077 ATCATTGATAAATTGAATTTATACCAATT 2106
                                                                                                                                                                                            641 TyrileAspLysileGluPheileProVal 650
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APPLICATION NUMBER: US/07/941,650A
FILING DATE: 19920908
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/758,020
FILING DATE: 12-ESP-1991
PRIOR APPLICATION NUMBER: US 07/658,935
FILING DATE: 21-FEB-1991
PRIOR APPLICATION NUMBER: US 07/654,112
FILING DATE: 16-JAN-1991
APPLICATION NUMBER: US 07/642,112
FILING DATE: 16-JAN-1991
ATTORNEY/AGENT INPORMATION:
NAME: SALIWANCHIN, DAVIG R.
REGISTATION NUMBER: 31,794
TELECOMMUNICATION NUMBER: 31,794
TELECOMMUNICATION NUMBER: 31,794
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                                                                                                                                                                                                                                                                                Sequence 4, Application US/07941650A; Patent No. 6294184; GENERAL INFORMATION:
                                                                                              2041 ATATTTAATCGTGCAGAT-
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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LOCATION: 1..651
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US-07-941-650A-4
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                                                                                                                                                                                                                                                                                                                                           CCCACACAAAAACTTTAATACCATTTGAATCCTATAAAGTTTCAATTGTAACTGATAGA 1335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1585 TATAAAATTGGATTAGCGCTAAATATATTATATACAGGTGCATTAGGATGGACACACAGT 1644
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                                     1129 CTTAGAȚTAȚTȚTCATTTTAGATGAACTTATAȚȚȚTATACAAAA-------- 1173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1336 CAAGTA-----ACTCCTACTTCCCCTTTTCCTAAC-----ATATACTTTACAATTAAT 1383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1384 CAAATTGAACTTTATTTAAATAATTCACCTAGTAATAAATTA-----ACATATTCA 1434
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                                                                                                                                                                                                                                                                                                                                                                                                                                     314 AlaLeuGlnGluTyrGlyProThrPheSerSerIleGluAsnSerIleArgLysPro--- 332
                                                                                                                                                                                                              ||||||| :::||| :::||| :::||| 333 ---HiaLeuPheAspTyrLeuArgGlyIyr 351
                                                                                                                                                                                                                                                                                                      352 SerGlyLy8AspSerPheAsnTyrTrpSerGlyAsnTyr-----ValGluThrArg 368
                                                                                                                                                                                                                                                                                                                                                                 ||| || || || || || || 369 ProSerIleGlySerAanAapThrIleThrSerProPheTyrGlyAapLyaSerIleGlu 388
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500 SerValAspPhePheAsnThrIleAspAlaGluLysIleThrGlnLeuProValValLys 519
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281 IleValLeuPheProPheTyrAspValArgLeuTyrSerLys-----
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621 SerGlyAepThrAenAepPheIleIleGlyAlaGluSerPheValSerAenGluLyeIle 640
1987 TAT-----TICCAATTICCAAGTACAGTACATTACCTTTAAATCGAAACATAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Uyeda, Kendrick A.
APPLICANT: Bradfisch, Gregory A.
TITLE OF INVENTION: Process for Controlling Lepidopteran Pests
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: David R. Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IMMEDIATE SOURCE:
CLONE: E. coli XL1-Blue (pM1,98-4), NRRL B-18291
FEATURE:
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	TATCTTAT erGluLeu	ATCAACCA snSerThr	AATATGGT hr	GTACTATT yileser	CGATAGGA ::: ValPro	CCGCGGGA ::: roser	TTGATACA :: leAspLys	GACAAATA :: :InAsnAsn	AAGCTCCT	GATTTGAG euPheSer	ATAAAACG ::::: heGluVal	AACAAGGT :: ysAspAla	CTAATGCT	CTAAATAT ::: ilnGlnTyr	AACCTAAT SerThrTyr	TAGATACT euAspLeu
	GTGATCAAAATAATAATAATGAATATGAGATTATCGATTCAAAGAATTAATCTTAT ::: ::: ::: :::	CCTTCTAACAGAAATATTGATCATTCTAGATACCCTTACACAAATAATCCAAATCAACA ::: ::: 	TTACAAAACACAAATTACAAAGAGTGGCTCAATATGTGTCAAGGGAATACACAATATGGT :::	dararttogagacatttgctagtgctgatacaattgctgcagttagtgcaggtactatt	GTATCCGGTACTCTGTTAGCCGGTATAGGTGGGCTCACTTCTATATCCGGACCGATAGGA 	ATAATAGGTGCTATAATAATATTTTTGGTACCCTAATCACTGTCTTTTGGCCCGGGGA	GAACAAGACAAAACAGTATGGACACAATTTATAAAATGGGAGAAATTTTTGTTGATACA	CCGTTAACAGAAAGCATAAAACAGCTAAAGTTACAAACTTTAGAAGGATTTAGACAAATA	TTACAAAGCTATAATACAGCATTAGATGATTGGAGAAAATTAAAAAGCTACAAGCTCCT ::	GGATTACCACCATCATCAGCATTACAACAAGCTGCCTTGACTTTAAAATACGATTTGAG 	AATGTTCACAATGATTTTATTCGAGAAATACCTGGTTTCCAACTTGAAACTTATAAAGG .:: .::	CTATTACTACTATTTATGCGCAAGCTGCTAATTTTCATTTAAATTTATAACAACAGGT 	GCTGAATTGGCTGATGGAATGCAGATATACATCCTTCACAAATTGAACCTAATGCT ::: GlnValpheglyGluGluTrpGlyTyr	GAACATCAGATGACTATTATAAACTTTTAAAAGAAAATATATACCTAAATAT ::: SerSerGluAspIleAlaGluPheTyrGlnArgGlnLeuLysLeuThrGlnGlnTyr	agtaactattgtgcaaatacctatagagagactaaataaa	ATGAGATGGAGTATATTAATGATTATCGAAGATATATGACTATTACTGTATTAGATACT
651 216 e: 116 270 148 31	, GATT LysValT	TACACAA : LeuAlaa	TGTCAAG Thralaa	GCTGCAG ABPAlaV	ACTTCTA	ATCACTG	ATGGGAG GlnValG	ACTTTAG : GlubeuG	AAATTAA Lys	TTGACTC	TTCCAAC	CATTTA	CCTTCAC	TTAAAAC ; jGlnLeuI	AATAAAC AsnSeri	ratgactz MetThri
Length: Matches: Conservative Mismatches: Indels: Gaps:	AGATTATC	GATACCT :: ilnTyrPro	TCAATATG	ATACAATT hrvallys	GTGGGCTC	GTACCCTA	TTATTAAA ::: heMetala	AGTTACAA \laLeuAla	ATTGGAGA ::: erTrpLye	CAAGCTGCC	ATACCTGGT ::: detProSer	SCTAATTT \alaasnTh	BATATACA	rataaacti ::: yrglnarg	BAAGGACTZ Valglyber	CGAAGATA) hrgarggl
Lengti Match Conse Misma Misma Indeli Gaps:	TGAATATG	TCATTCTP :::: -HisAsnG	AGAGTGGC ::: sGluPhel	TAGTGCTC ::: pSerSer1	CGGTATAC ::: yvalvalC	ATCTTTTG :::	GACACAAT	ACAGCTA? '8SerLys?	ATTAGATC	ATTACAAC :::: :gSerArg?	TCGAGAA	GCAAGCTC	GAATGCAC pglytyr	TAT. ::: laGluPhe'	CTATAGA pTyrasn'	ATGATTATO ::: anArgPhe
1.37e-55 706.00 44.27% 28.80% 17.92%	raaraaraa aasnargse	AATATTGA	AATTACAA ABNTYTLY	ACATTTGC ValleuAs	GTATCCGGTACTCTGTTAGCCGGTATAGGT 	FATAATAAT : : : aLeuThrSe	AACAGTATG	AAGCATAAA - -	raaracago - rvalasnal	ATCATCAGC ::: lAsnLeuAr	rGATTTTAT : :HisPheA	TATTTATGO	GCTGAATTGGCTGATGAATGGAATGCAG GlnvalpheGlyGluGluTrpGlyTyr-	TGAC : uABpileA]	TGCAAATA(8ValAenTi	TATATTTA LysPheA
	ATCAAAA:	CTAACAG	AAAACAC :: luglule:	ATTTCGA(CCGGTAC alGlyGl:	TAGGTGC	AAGACAA Aspal	TAACAGA	AAAGCTA:	TACCACC	TTCACAA	TACTACC	AATTGGC	GGAACATCAGATGAC ::: ::: SerSerGluAspIl	ACTATIG ::::: \BPH!8Cy	AGATGGAG \laTrpVa
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ment Scores: No.: It Similarity Local Similar Match:	1 1	58	118	178	238	298	358 103	418	478	538	598	658	718	778	829	889
Alignment Scores: Pred. No.: Score: Percent Similarity: Best Local Similarity Dery Match:	2 2 3 3 4 8	& 8	ጵ	ጵ ය	& 93 18	ራ 8	8 & 8	<u>\$</u> 8	<u>ጽ</u>	දු දු	දු දු	중 A	දු පු	ጵ	& a	<u>ئ</u> ۾

949	9 ATCGCTCAATTTTCTTTTTATGATATAAGAGATACAAAGATTCAATAGGAAGAATAGGT 1 	1008 294
1009	GGCATTAAAACTGAACTTACAAGAGAAATTTATACAACTGAAATAAAT	1068 313
1069	9 ACTTACCTTGAAATTTCAACCCAATCTCGCTATAATGGAATATAATTTAACACGTTCAGGG 1	1128 332
1129	9 CTTAGATTATTTTCATTTTTAGATGAACTTATATTTTTATACAAAA	1173 351
1174	4	1215 368
121	6 AATAGATCTACTTATGCTACGACAGGAACTGAAATTATATATGGAGAAAGAA	1275 388
127	cccacaacaaaaactitaataccatitgaatcctataaagtitcaatigtaactgataga 1 	1335
133	6 CAAGTAACTCCTACTTCCCTATTTCCTAACATATACTTTACAATTAAT 1	1383 422
138,	4 CAAATTGAACTTTATTTAAATAATTCACCTAGTAATAATTAACATATTCA 1	1434
143	5 GCTGGGGGGAATTTATCTAATGATAAAAAA 1::	1464 462
1465	5 ACAACTGATTTTCAATTTCCTGTAAAAAAGACTGTAAACCAATTATTAATCCAAATTGT 1 3 ThrThrAspGluProLeuGluLys	1524 470
1525	S TTACCAAGCTATAATAATTATAGTCATATTTTATCCCAGTTTTCTTTATTTA	1584 485
158	5 TATAAAATTGGATTAGCGCTAAATATATTATACAGGTGCATTAGGATGGACACACAGT 1	1644 499
164!	S AGTGTTAATAGAAATAATGCAATATCAGATAAAATAATTACAATGATCCCAGCAATCAAA 1	1704 519
170	5 GGTAACAGTCTTGATACAAACTCTAAGGTAATTGAAGGACCTGGTCATACAGGAGGAAAC 1 ::	1764 539
176 54	5 TTGGTTTATTTACAAAGTCAAGGGCGTTTAGAGATTACATGTAGAACT 1	1812 559
181.	3 CCTAATICTACACATCTTATTACATTAGACTICGATACGCTACAAATGGTGCTGGAAAT 1	1872 575
1873	3 ACTCTTCCTAATATATCTCTTACAATACCAGGAGTAATAGGAATACCACCTCAACGACTC	1932

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949 ATCGCTCAATTTTCTTTTTATGATATAAAGAGATACAAAGATTCAATAGGAAGAATAGGT 1008
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                                                                                                                                                                                                                                                                                                                                                                                                                                       -----AspAlaAspProTrpLysAlaPheMetAlaGlnValGluValLeuIleAspLys 128
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                                                                  CCTTCTAACAGAAATATTGATCCATTCTAGATACCCTTACACAAATAATCCAAATCAACCA 117
                                                                                                                                   118 TTACAAAACACAAATTACAAAGAGTGGCTCAATATGTGTCAAGGGAATACACAATATGGT 177
                                                                                                                                                                                                                                                                         GTATCCGGTACTCTGTTAGCCCGGTATAGGTGGGCTCACTTCTATATCCGGACCGATAGGA 297
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80 ValValGlyGlnIleLeuGlyValValGly-----------ValPro 91
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MetasnProAsnAsnArgSerGluTyrAspThrIleLysValThrProAsnSerGluLeu
                                                                                      GATAATTTCGAGACATTTGCTAGTGCTGATACAATTGCTGCAGTTAGTGCAGGTACTATT
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   GTGAATCAAAATAATAATGAATATGAGATTATCGAT---TCAAAGAATTTATCTTAT
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                                                                 TAT-----TICCAATTICCAAGTACAGTAACATTACCTTTAAATCGAAACATACCATTT 2040
                                                                                                                                  ------GTATCAATTCAATTTTA 2076
AACAACACTTTTTCTGGTACAAATTATAATAATTTACAATAC-----GGAGATTTTGGG 1986
                                                                                    ||| |||::: |||
-----AsnSerAsnMetGlyPhe 620
                                                                                                                                                                 621 SerGlyAspThrAsnAspPhellelleGlyAlaGluSerPheValSerAsnGluLysIle 640
                             586 AsnAsnAspPheleuVallleTyrIleAsnLysThrMetAsnIleAspGlyAspLeuThr 605
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/996,441B
FILING DATE: 18-DEC-1997
CLASSIPICATION: 800
ATTORNEY/AGRAT INFRAMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REGISTRATION NUMBER: 33,928
REGISTRATION NUMBER: MECO:151
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
TELEPHONE: 512/418-300
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                                                                                                                                                                                    2077 ATCATTGATAAATTGAATTTATACCAATT 2106
                                                                                                                                                                                                                    641 TyrlleAspLyslleGluPhelleProVal 650
                                                                                      ADDRESSEE: Arnold, White & Durkee STREET: P.O. Box 4433
CITY: Houston STARE: Texas
COUNTRY: USA
                                                                                                                                  1041 ATATTTAATCGTGCAGAT-----
                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Kulesza, Caroline A. APPLICANT: Walters, Prederick S. APPLICANT: Slatin, Stephen L. APPLICANT: Von Tersech, Michael A. APPLICANT: Romano, Charles TITLE OF INVENTION: INSECT-RESISTAN NUMBER OF SEQUENCES: 113
                                                                                                                                                                                                                                                                                                     Sequence 112, Application US/08996441B
Patent No. 6023013
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                      English, Leigh H.
Brussock, Susan M.
Malvar, Thomas M.
Bryson, James W.
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INPORMATION FOR SEQ ID NO: 112:
SEQUENCE CHARACTERISTICS:
LENGTH: 659 amino acids
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amino acid
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44.27%
28.80%
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ADDRESSEE: Arnold, W
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
COMPUTER: IBM PC COM
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APPLICANT:
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629 SerGlyAspThrAsnAspPhellelleGlyAlaGluSerPheValSerAsnGluLysIle 648
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9 MetAsnProAsnAsnArgSerGluTyrAspThrIleLysValThrProAsnSerGluLeu
                                                                                                                                                                                                                 APPLICANT: Bryson, James W.
APPLICANT: Kulesza, Caroline A.
APPLICANT: Walters, Prederick S.
APPLICANT: Walters, Prederick S.
APPLICANT: Slatin, Stephen L.
APPLICANT: Non Tersch, Michael A.
APPLICANT: Romano, Charles
TITLE OF INVENTION: UCLEIC ACID SEGMENTS ENCODING MODIFIED
TITLE OF INVENTION: COLEOPTERAN-TOXIC CRYSTAL PROTEINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
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216
116
270
31
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
APPLICATION NOATA:
APPLICATION NUMBER: US/08/993,722A
FILING DATE: 18-DEC-1997
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Matches:
Conservative:
Mismatches:
Indels:
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                                2077 ATCATTGATAAATTGAATTTATACCAATT 2106
                                               649 TyrileAspLysileGluPheileProVal 658
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NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: MECO:149
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3106
TELEFAX: 512/474-7577
                                                                                                                        ; Sequence 112, Application US/08993722A
; Patent No. 6060594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO: 112:
SEQUENCE CHARACTERISTICS:
LENGTH: 659 amino acids
                                                                                                                                                                                    Brussock, Susan M.
Malvar, Thomas M.
Bryson, James W.
                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: English, Leigh H.
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706.00
44.27%
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amino acid
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CITY: Houston
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MEDIUM TYPE: Floppy
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                                                                                            RESULT 9
US-08-993-722A-112
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APPLICANT:
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451 SerLyBārgTyrāsnGlyTyrLeuGlyālaGlnāspSerIleāspGlnLeuProProGlu 470
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 322 AlaLeuGlnGluTyrGlyProThrPheSerSerIleGluAsnSerIleArgLysPro--- 340
                                                                                                                                         360 SerGlyLysAspSerPheAsnTyrTrpSerGlyAsnTyr-----ValGluThrArg 376
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568 AlaAlaLeuLeuGlnArgTyrArgValArg1leArgTyrAlaSerThr------
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45	360 SerGlyLyBABpSerPheAsnTyrTrpSerGlyAsnTyrValGluThrArg	OY 1216 AATAGATCTATGCTACGACAGGAACTGAAATTATATATGGAGAAAGACAGTCCA 1275	OY 1276 CCCACAACAAAACTTTAATACCATTTGAATCCTATAAAGTTTCAATTGTAACTGATAGA 1335	Oy 1336 CAAGTAACTCCTACTTCCCTTTTCCTAACATATACTTTACAATTAAT 1383 Db 11 ThrileAlaAsmThrAspIleAlaAlaPheProAspGlyLysIleTyrPheGlyValThr 430	Qy 1384 CAAATTGAACTTTATTTAAATTACACCTAGTAATAATTAACATATTCA 1434	Qy 1435 GCTAAA 1464 :::	OY 1465 ACAACTGATTTTCAATTTCCTGTAAAAAAGACTGTAAACCAATTATTAATCCAAATTGT 1524	OY 1525 TTACCAAGCTATAATAGTTATAGTCATATTTTATCCCAGTTTTCTTTATTTA	Qy 1585 TATAAAATTGGATTAGGGCTAAATATATATAGGGGGGGTTAGGATGGACACACAGT 1644 Db 494 AspArgArgGlyThr11eProPhePheThrTrpThrHisArg 507	Qy 1645 AGTGTTAATAGAAATAATGCAATATGCAGTAAAATAATTACAATGATGCCAGGAATCAAA 1704	OY 1705 GGTAACAGTCTTGATACAAACTCTAAGGTAATTGAAGGACCTGGTCATACAGGAGGAAC 1764	Oy 1765 TTGGTTTATTACAAAGTCAAGGGGGTTTAGAGATTACATGTAGAACT 1812	Qy 1813 CCTAATTCTACACTATTACATTAGACTTCGATACGCTACAAATGGTGCTGGAAAT 1872	OY 1873 ACTCTCCTAATATATCTCTTACAATACCAGGAGTAATAGGAATACCACCTCAACGACTC 1932	Qy 1933 AACAACACTTTTTCTGGTACAAATTATAATATTTACAATACGGAGATTTTGGG 1986	QY 1987 TATTICCAATITCCAAGTACAGTAACATTACCTITAAATCGAAACATACCATTT 2040 DD	Qy 2041 ATATTTAATCGTGCAGAT	Qy 2077 ATCATTGATAAAATTTGAATTTATACCAATT 2106 	RESULT 10 US-08-993-170A-112 ; Sequence 112, Application US/08993170A
		ACTATT	GTATCCGGTACTCTGTTAGCCGGTATAGGTGGGCTCACTTCTATATCCGGACCGATAGGA		GAACAAGACAAAACAGTATGGACACAATTTATTAAAATGGGAGAAATTTTTGTTGATACA	47	LysileGludluTyrAlaLysSerLysAlaLeuAlaGluLeuGlnGlyLeuGlnAsnAsn TTACAAAGCTATAATACAGCATTAGATGATAGAGAAAATTAAAAAGACTACAAGCTCCT TACAAAGCTALAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	GGATTACCACCATCATCAGCATTACAACAAGCTGCCTTGACTCTTAAAATACGATTTGAG	Ateriovalmentigserrightsercinabpatglieargglubenbeser Aatgricacaatgattitattcgagaaatacctggttrccaacttgaaacttataaaacg ::::	CTATTACTACTATTTATGCGCAAGCTGCTAATTTTCATTTAAATTTTATACAAGGT	Deurnebeurtoinriyralaginalaalaasninrhisbeeuleuleulysaspala GCTGAATTGGCTGATGAATGGAATGCAGATATACATCCTTCACAAATTGAACCTAATGCT	GGAACATCAGATGACTATTATAAACTTTTAAAAGAAAATATACCTAAATAT :::[::: :::	sersergiumbpliemiagurneryrginmiggginneulysbeutnikginginiyr AGTAACTATTGTGGAAATACCTATAGAGAGGACTAAATAAA	ATGAGATGAGTATATTAATGATTATCGAAGATATATGACTATTACTGTATTAGATACT ARABIATTAGATTAATGATATCGAAGATATATGACTATTACTGTATTAGATACT ARABIATTAGATTAATGATAATGAGATATATGACTATTACTGTATTAGATACT ARABIATTAGATAGATAATGAGATAATGAGAGATAATGAGAGATAATGAGATAATGAGAGATAATGAGATAATGAGATAATGAGATAATGAGATAATGAGATAATGAGAGATAATGAGAGATAATGAGAGATAATGAGAGATAATGAGAGATAATGAGAGATAATGAGAGATAATGAGAGATAATGAGAGATAATGAGAGAGAATAAT	ATGCTCAATTTTTTTTTTTTATGATATAAGAGATACAAGAGATTCAATAGGAAGAATAGGT	GGCATTAAAACTGAACTTACAAGAAATTTATACAACTGAAATAAAT	ACTTACCTTGAAATTCAACCCAATCTCGCTATAATGGAATATAATTAACACGTTCAGGG	ALALBUGINGINITYISIYPEOINTENBESEKSEKIIGGINABNSGKIILGAKGLYBFYO CTTAGATTATTTTCATTTTTAGATGAACTTATATTTTATACAAAA	

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1174 ------AATGAAACGTACGGAATCGTTTAGTTGCGAATCGT 1215
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                                                             298 ATAATAGGTGCTATAATAATATCTTTTGGTACCCTAATCACTGTCTTTTGGCCCGCGGGA 357
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PheAlaGlyAlaLeuThrSerPheTyrGlnSerPheLeuAsnAlaIleTrpProSer---
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230 ---SerSerGluAspIleAlaGluPheTyrGlnArgGlnLeuLysLeuThrGlnGlnTyr
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                                                                                                                                                                       GGATTACCACCATCATCAGCATTACAACAAGCTGCCTTGACTCTTAAAATACGATTTGAG
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|LeuGluLeuAsnTyrLysGluPheLeuArgMetThrAlaAspAsnSerThr---- 62
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-----GluValLeuAspSerSerThrValLysAspAlaValGlyThrGlyIleSer
GENERAL INPORMATION:

GENERAL INPORMATION:

APPLICANT: English, Leigh H.

APPLICANT: Brussock, Susan M.

APPLICANT: Brussock, Susan M.

APPLICANT: Malvar, Thomas M.

APPLICANT: Malvar, Thomas M.

APPLICANT: Walters, Frederick S.

APPLICANT: Walters, Frederick S.

APPLICANT: Walters, Prederick S.

APPLICANT: Walters, Stephen L.

APPLICANT: Walters, Stephen L.

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APPLICANT: Stephen L.

APPLICANT: Walters, Stephen L.

APPLICANT: Stephen L.

APPLICANT: Walters, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READBLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPARING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/993,170A
FILING DATE: 18-DEC-1997
CLASSITCATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REGISTRATION NUMBER: 33,928
REFERENCE/OPCKET NUMBER: 33,928
REFIRENCE/OPCKET NUMBER: 33,928
TELERPHONINICATION INFORMATION:
TELERPHONIN: 512/418-3000
TELERPAX: 512/474-7577
INFORMATION FOR SEQ ID NO: 112:
SEQUENCE CHARACTERISTICS:
LENGTH: 659 amino acids
THENGTH: 659 amino acids
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Conservative:
Mismatches:
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Best Local Similarity:
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92 PheAlaGlyAlaLeuThrSerPheTyrGlnSerPheLeuAsnAlaIleTrpProSer--- 110
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| ProThrAsn------HisAsnGlnTyrProLeuAlaAspAsnProAsnSerThr 44
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|LeuGluGluLeuAsnTyrLysGluPheLeuArgMetThrAlaAspAsnSerThr----
 METHODS FOR IMPROVING THE ACTIVITY OF DELTA-ENDOTOXINS AGAINST INSECT PESTS
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APPLICATION NUMBER: US/08/993,775B
FILING DATE: US-1997
CLASSIFICATION: 514
ATTONREY/AGET INFORMATION:
NAME: Ktchell, Barbara S.
REGISTRATION NUMBER: 33,928
REGISTRATION NUMBER: 33,928
TELEPRATION NUMBER: 33,928
TELEPRATION NUMBER: 33,928
TELEPRATION NUMBER: 31,928
TELEPRATION STATEMENTION: TELEPRATION: TELEPRATION: TELEPRATION: 512/418-3000
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Matches:
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                                                                 ADDRESSEE: Arnold, White & Durkee STREET: P.O. Box 4433 CITY: Houston STATE: Texas COUNTRY: USA
                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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INFORMATION FOR SEQ ID NO: 112:
SEQUENCE CHARACTERISTICS:
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TITLE OF INVENTION: DE
TITLE OF INVENTION: DE
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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MEDIUM TYPE: Floppy
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US-08-993-775B-112
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Best Local Similarity:
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1336 CAAGTA-----ACTCCTACTTCCCCTTTTCCTAAC-----ATATACTTTACAATTAAT 1383
                                                                      CAAATTGAACTTTAATTAAATAATTCACCTAGTAATAAATTA------ACATATTCA 1434
                                                                                                                                           GCT------AAA 1464
                                                                                                                                                                                                                  ACAACTGATTTTCAATTTCCTGTAAAAAAAGACTGTAAACCAATTATTAATCCAAATTGT 1524
                                                                                                                                                                                                                                                                                       1585 TATAAAATTGGATTAGCGCTAAATATATATATACAGGTGCATTAGGATGGACACACAGT 1644
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                      ::: |||| ::: |||| ::: |||||||| ::: ThrileAlaAsnThrAspIleAlaAlaPheProAspGlyLysIleTyrPheGlyValThr 430
                                                                                                                                                                             451 SerLysArgTyrAsnGlyTyrLeuGlyAlaGlnAspSerIleAspGlnLeuProProGlu 470
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                                                                                                                                                                                                                                                                                                                                                                                             494 AspArgArgGlyThrIle-----ProPhePheThr------TrpThrHisArg 507
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LysValAspPheSerGlnTyrAspAspGlnLysAsnGluThrSerThrGlnThrTyrAsp
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|LeuLeuPheLeuLysGluSerSerAsnSerlleAlaLysPheLysValThrLeuAsnSer
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APPLICANT: Brussock, Susan M.
APPLICANT: Brussock, Susan M.
APPLICANT: Malvar, Thomas M.
APPLICANT: Bryson, James W.
APPLICANT: Kulesza, Caroline A.
APPLICANT: Walters, Frederick S.
APPLICANT: Slatin, Stephen L.
APPLICANT: Von Tersch, Michael A.
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US-08-993-775B-112
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Db 451 SerLysArgTyrAsnGlyTyri Qy 1465 ACAACTGATTTCCATTTCCTC	Qy 1645 ACTGTTAATAGAAATAATGCAA Db 508 SerValAspPhePheAsnThr: Qy 1705 GGTAACAGTCTTGATACAACA Qy 1765 TTGGTTTATTTACAA Qy 1813 CCTAATTCTACAA Qy 1813 CCTAATTCTACACAATTTATT Qy 1813 CCTAATTCTACACAATTTATT Qy 1873 ACTCTCCTAATAATTCTTATT Qy 1873 ACTCTTCCTAATAATATCTCTT Qy 1873 ACTCTTCTCTAATAATATCTCTT Qy 1833 ACACACATTTTCTGGTACA Qy 1933 ACACACATTTTTCTGGTACA Qy 1933 ACACACATTTTTCTGGTACA Qy 1934 AsnAsnAspPeLeuvallle'	Qy 1987 TATTTCCAATTTCAA	GEMERAL INFORMATION: APPLICANT: Brussock, Susan M. APPLICANT: Brussock, Susan M. APPLICANT: Brussock, Susan M. APPLICANT: Bryson, James M. APPLICANT: Kulesza, Caroline J. APPLICANT: Walters, Frederick APPLICANT: Walters, Frederick APPLICANT: Won Tersch, Michael TITLE OF INVENTION: NUCLESTE AFTITE OF INVENTION: NUCLESTE AFTITE OF INVENTION: NUCLESTE AFTITE OF INVENTION: OLEOPTER NUMBER OF SEQUENCES: 113 CORRESPONDENCE ADDRESS: ADDRESSES: Arnold, White & J. STREET: P.O. Box 4433 CITY: Houston STATE: Texas COUNTRY: USA
	CTATTACTACCTATTATGGCAAGCTCTAATTTCATTTAATTTACAACAAGGT LEUPheLeuProthriytatgGCAAGCTCCTAATTTCATTTAATTTACAACAAGGGT LEUPheLeuProthriytatgGCAAGCTCCTAATTTTCATTTAATTTAATTTACAACAAGGT LEUPheLeuProthriytatgGAATGCAAGTATACATTCACAAATTGAACCTAATGCT SISSIMALING SATURATAAACTTTTAAAAATTACAAATTACAATGCT GAACATCAATGAATGCAATACAAATAAACTTTTAAAAAAAA	289 IleValLeuPheProPheTyrAsgValArgLeuTyrSerLys 302 1009 GGCATTAAAACTGAACTTACAAGAGAATTTATACAACTGAAATAATTTTGACCGTCTT 1068 303 GlyValLygThrGluLeuThrArgAsgIlePheThrAsgProIlePheThrLeuAsn 321 1069 ACTTACCTTGAATTCAACCCAATCTGCTATAATGAATATAATTTAACACGTTCAGGG 1128 322 AlaLeuGlnGluTyrGlyProThrPheSerSerIleGluAnnSerIleArgLygBro 340 1129 CTTAGATTATTTTGATTTTTAAATGAACTTTAAACAAAA	
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ellelleGlyAlaGluSerPheValSerAsnGluLysile 648
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uPheVal------GinAsnSer 593
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249 ThraspHisCysValAsnTrpTyrAsnValGlyLeuAsnSerLeuArgGlySerThrTyr 268
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---HisLeuPheAspTyrLeuArgGlyIleGluPheHisThrArgLeuArgProGlyTyr 359
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---SerSerGluAspileAlaGluPheTyrGlnArgGlnLeuLysLeuThrGlnGlnTyr
       GGATTACCACCATCATCAGCATTACAACAAGCTGCCTTGACTCTTAAAATACGATTTGAG
                                                                                                              GlnAlaGluSerHisPheArgAsnSerMetProSerPheAlaValSerLysPheGluVal
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|PheAlaGlyAlaLeuThrSerPheTyrGlnSerPheLeuAsnAlaIleTrpProSer--- 110
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-----AspAlaAspProTrpLysAlaPheMetAlaGlnValGluValLeulleAspLys 128
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LysIleGluGluTyrAlaLysSerLysAlaLeuAlaGluLeuGlnGlyLeuGlnAsnAsn 148
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|FeuGluGluLeuAsnTyrLysGluPheLeuArgMetThrAlaAspAsnSerThr----
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Matches:
Conservative:
Mismatches:
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                                                                                                                                      CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRILING DATE:
FILING DATE: 18-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: MECO:149
TELECOMUNICATION INFORMATION:
TELEFRONE: 512/448-7577
INFORMATION FOR SEQ ID NO: 112:
SEQUENCE CHARATERISTICS:
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: PACENTIN Release #1.0, Ve
CURRENT APPLICATION DATA::
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706.00
44.27%
28.80%
17.92%
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TYPE: amino acid
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Best Local Similarity:
Query Match:
DB:
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Matches:
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Mismatches:
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        CORRENT AFELLICATION DATE:

PILING DATE:
CLASSIFICATION:
PRICA APPLICATION:
PRICA APPLICATION:
APPLICATION NUMBER: 08/993,722
PILING DATE:
ATTORNEY/AGENT:
NAMB: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REGISTRATION NUMBER: 33,928
REGISTRATION NUMBER: 33,928
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: MECO:149
TELEPHONE: 512/418-3106
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INFORMATION FOR SEQ ID NO: 112:
SEQUENCE CHARACTERISTICS:
LENGTH: 659 amino acids
TYPE: amino acid
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44.27%
28.80%
17.92%
CURRENT APPLICATION DATA
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                                                                                                                              AGTGTTAATAGAAATAATGCAATATCAGATAAATAATTACAATGATCCCAGCAATCAAA 1704
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-----ThrAsnLeuArgLeuPheVal-------GlnAsnSer 593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ::: |||||||| ::: 629 SerGlyAspThrAsnAspPhellelleGlyAlaGluSerPheValSerAsnGluLysIle 648
                                                                                   ::: ||| || || || || 494 AspargargdlyThrIle-----ProPhePheThr------TrpThrHisArg 507
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                    ||||::::::|||:::
| LeuLeuPheLeuLysGluSerSerAsnSerIleAlaLysPheLysValThrLeuAsnSer
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568 AlaAlaLeuLeuGlnArgTyrArgValArgIleArgTyrAlaSerThr------
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Patent No. 6642030

GENERAL INFORMATION:

APPLICANT: Brussock, Susan M.

APPLICANT: Brussock, Susan M.

APPLICANT: Malvar, Thomas M.

APPLICANT: Walters, Frederick S.

APPLICANT: Walters, Frederick S.

APPLICANT: Slatin, Stephen L.

APPLICANT: Somano, Charles

TITLE OF INVENTION: COLEOPTERAN-TOXIC CRYSTAL PROTEINS

WANTHIN OF INVENTION: COLEOPTERAN-TOXIC CRYSTAL PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOPTWARE: PatentIn Release #1.0, Version #1.30
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STREET: P.O. Box 4433
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, W
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STATE: Texas
COUNTRY: USA
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US-09-427-769-112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            ------GluvalLeuAspSerSerThrvalLysAspAlavalGlyThrGlyIleSer 79
                                  29 ProThrAgn------HisaanGlnTyrProLeuAlaaspAsnProAsnSerThr
                                                                                                                                                                                                                                                                                                      GTGAATCAAAATAATAATGAATATGAGATTATCGAT---TCAAAGAATTTATCTTAT
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Db 494 AspArgArgGlyThrIleProPhePhe Qy 1645 AGTGTTAATAGAAATAATGCAATATCAGATAAA Db 508 SerValAspPhePheAsnTrIleAspAlaGlu Qy 1705 GGTAACAGTCTTGATACAACTCTAAGGTAATT Db 528 AlaTyTATTACAAAGTCAA Qy 1765 TTGGTTATTACAAAGTCAA Db 548 LeuLeuPheLeuLysGluSerSerAsnSerIle Qy 1813 CCTAATTCTACAAAGTCAA Db 568 AlaAlaLeuCaATCTTATTACATTACATTAGACTT Db 568 AlaAlaLeuLeuGlnArgTyZATGAATGIle	Qy 1873 ACTCTTCCTAATATATCTCTTACAATACCAGGA Db 584ThrAshLeuArgLeuDheVal Qy 1933 AACAACACTTTTTCTGGTACAAATTATAATAATAATAATAATAATAATAATAATAAT	2,25	COUNTY: USA ZIP: 77210 COMPUTER READBLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS GOFTWARE: Patentin Release #1.0, Versic CURRENT APPLICATION DATA: PTLING DATE: 18-DEC-1997 CLASSIFICATION: 800 ATTORNEY/AGENT INFORMATION: NAME: Kitchell, Barbara S. REGISTRATION NUMBER: 33,928
181 GlnalaGluSerHisPheArgAsnSerMetProSerPheAlaValSerLysPheGluVal 200 658 CTATTACTACCTATTATGGCAAGCTGCTAATTTTCATTAAATTTATACAACAAGGT 717 [1	249 ThrasphiscysvalashTrpiyrashvalGlyLeuAshSerLeuArgGlySerThrTyr 268 889 ATGAGATGGAGTATATTAATGATATATCGAGATATATGATATTACTGTATTAGTACT 948 269 AspalaTrpvalLysPheAshargargGluMetThrLeuThrValLeuAspLeu 288 949 ATGGCTCAATTTTCTTTTTATGATATAAAGGATACAAAGATTCAATAGGAAGAATAGGT 1008	SerGlyLysAspSerPheAsnTyTTrSerGGAATGGTTAGGGAATGGT	1435 GT
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AAGGCCTTTACAGATTACATGTAGAACT 1812
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leAlaLysPheLysValThrLeuAsnSer 567 TTCGATACGCTACAAATGGTGCTGGAAAT 1872 ::||||||||||::: leArgTyralaSerThr----- 583 ATTTACAATAC-----GCAGATTTTGCG 1986 CATTACCTTTAAATCGAAACATACCATTT 2040 ------GTATCAATTCAATTTTA 2076 AAATAATTACAATGATCCCGGCAATCAAA 1704 :: ||||| ::||| :uLysileThrGlnLeuProValValLys 527 TTGAAGGACCTGGTCATACAGGAGAAAC 1764 GAGTAATAGGAATACCACCTCAACGACTC 1932 neThr-----TrpThrHiBArg 507 ANSGENIC PLANTS ion #1.30 2106 658

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|LeuGluGluLeuAsnTyrLysGluPheLeuArgMetThrGluAspSerSerThrGluVal
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| ProThrAsn------HisAsnGlnTyrProLeuAlaAspAsnProAsnSerThr
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Ser-----AspalaAspProTrpLysAlaPheMetAlaGlnValGluValLeuIle
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216
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272
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Matches:
Conservative:
Mismatches:
Indels:
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     MBC0:151
REFERENCE/DOCKET NUMBER: MECO:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
TELEPHONE: 512/418-3000
TELEPHONE: 512/418-7577
INFORMATION FOR SEQ ID NO: 110:
SEQUENCE CHARACTERISTICS:
LENGTH: 652 animo acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-996-441B-110
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700.00
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Best Local Similarity:
Query Match:
DB:
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464 ThrAsp-----GluProLeuGluLys--------
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                                                                                   832 AACTATTGTGCAAATACCTATAGAGAAGGACTAAAATAAACTTCGAAACGAACCTAATATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              315 LeuGlnGluTyrGlyProThrPheLeuSerIleGluAsnSerIleArgLysPro----
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444 LysArgAsnAsnGlyHisValGlyAlaGlnAspSerIleAspGlnLeuProProGluThr
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211 AspAlaGlnValPheGlyGluGluTrpGlyTyrSer----------- 222
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|LeuGluGluLeuAsnTyrLysGluPheLeuArgMetThrGluAspSerSerThrGluVal 56
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Matches:
Conservative:
Mismatches:
Indels:
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700.00
44.58%
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17.77%
  ; TOPOLOGY: linear
US-08-993-722A-110
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Best Local Similarity:
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GITTATTTACAA------AGTCAAGGCGTTTAGAGATTACATGTAGAACTCCT 1815
                                                                                          1816 AATTCTACAATCTTATTACATTAGACTTCGATACGCTACAAATGGTGCTGGAAATACT 1875
                                                                                                                                                                                      1876 CTTCCTAATATATCTCTTACAATACCAGGAGTAATAGGAATACCACCTCAACGACTCAAC 1935
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                          :::::|||:::
541 LeuPheLeuLysGluSerSerAsnSerIleAlaLysPheLysValThrLeuAsnSerAla 560
                                                                                                                                                                                                                                  ---ThrashLeuArgLeuPheVal--------GlnAshSerAsh 586
                                                                                                                                                                                                                                                                                                                            587 AsnAspPhelleVallleTyrIleAsnLysThrMetAsnIleAspAspAspLeuThrTyr 606
                                                                                                                                                                                                                                                                                                                                                                                                       561 AlaLeuLeuGlnArgTyrArgValArgIleArgTyrAlaSerThr-------
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NAT: Brussock, Susan M.

NAT: Brussock, Susan M.

NAT: Brussock, James M.

NAT: Kulesza, Caroline A.

NAT: Kulesza, Caroline A.

NAT: Saltin, Stephen L.

NAT: Von Tersch, Michael A.

NAT: Somano, Charles

PEINVENTION: COLEOPTERAN-TOXIC CRYSTAL PROTEINS
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CAMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/993,722A
FILING DATE: 18-DEC-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFFRENCE/DOCKET NUMBER: 33,928
REFFRENCE/DOCKET NUMBER: 31,928
REFERENCE/DOCKET NUMBER: MECO:149
TELECOMMULCATION INFORMATION:
TELEPHONE: 512/418-1106
TELEPHONE
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CITY: Houston
STATE: Texas
COUNTRY: USA
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US-08-993-722A-110
; Sequence 110, Application US/08993722A
; Patent No. 606994
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È	952	GCTCAATTTTCTTTTTATGATATAAAGAGATACAAAGATTCAATAGGAAGAATAGGTGGC 1011
QQ	282	ValLeupheProPheTyrAspValArgLeuTyrSerLysGly 295
ð 6	1012	ATTAAAACTGAACTTACAAGAGAAATTTATACAACTGAAATAAAT
l &		
쇰	315	
È	1132	AGATTATTTTTTTTTTTAGATGAACTTATATTTTATACAAAA
අ	333	HisbeupheAspTyrbeuGlnGlyIleGlupheHisThrArgLeuGlnProGlyTyrSer 352
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qo	370	:::
È	1279	ACAACAAAAACTTTAATACCATTTGAATCCTATAAGTTTCAATTGTAACTGATAGACAA 1338
qq	390	ValGlnLysLeuSerPheAspGlyGlnLysValTyrArgThr 403
ठे व	1339	GTAACTCCTACTTCCCCTTTTCCTAACATATACTTTACAATTAATCAA 1386 :::
e d	4 6	
충 음	1387	#TIGBACTTIATTIAAAIAATTCACCIAGIAAIAAAITAALAKIILAACI 143/ :::::: ValaappheSerGinTyraapaagGinLyaAanGluThrSerThrGinThrTyraapSer 443
ờ	1438	AAAACA 1467
qq	444	
È	1468	ACTGATTTTCAATTTCCTGTAAAAAAAGACTGTAAACCAATTATTAATCCAAATTGTTTA 1527
qq	464	 ThraspGluProLeuGluLys
ò	1528	CCAAGCTAIAATAGTUATAGTCATATTTTATCCCAGTTTTCTTTATTTAATTATTCCTAT 1587
qq Q	471	AlafyrserHisGlnLeuAsnTyrAlaGluCysPhereuMetGlnAsp 486
Š	1588	TTAGGATGGACACACAGTAGT
QQ Q	487	
è	1648	GITAATAGAAATAAGGAATATCAGATAAAATAACAATGATCCCAGCAATCAAAGGT 1707
ą	501	ValaspPhePheAsnThrIleAspAlaGluLysIleThrGlnLeuProValValLysAla 520
ò	1708	AACAGTCTTGATACAAACTCTAAGGTAATTGAAGGACCTGGTCATACAGGAGAAACTTG 1767
qq	521	TyralaieuserserglyalaserlleiledludiyProdiyPheThrdlydlyasnieu 540
ò	1768	
qq	541	LeuPheLeuLysGluSerSerAsnSerIleAlaLysPheLysValThrLeuAsnSerAla 560
È	1816	AATTCTACACAATCTTATTACATTAGACTTCGATACGCTACAAATGGTGCTGGAAATACT 1875
QQ	561	
à	1876	CTTCCTAATATATCTCTTACAATACCAGGAGTAATAGGAATACCACCTCAACGACTCAAC 1935

989	686	909	2040	523	2085	543		
::: ::: 576ThrAsnLeuArgLeuPheValGlnAsnSerAsn 586	1936 AACACTTTTTCTGGTACAAATTATAATAATTTACAATACGGAGATTTTGGGTAT 1989	 S87 AsnAspPhelleVallleTyrIleAsnLysThrMetAsnIleAspAspAspAspLeuThrTyr 606	TTCCAATTTCCAAGTACAGTAACATTACCTTTAAATCGAAACATACCATTT	607 GlnThrPheAspLeuAlaThrThrAsnSerAsnMetGlyPheSerGlyAsp 623	1AIATTTAATCGTGCAGATGTATCAAATTCAATTTTAATCATTGAT 2085	ThrAsnGluLeulleileGlyAlaG	2086 AAAATTGAATTTATACCAATT 2106	
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Search completed: January 12, 2006, 06:41:17 Job time : 88 secs

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